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FIGURE 1A

The Small Island: 10848bp (SEQ ID NO: 1)

TTTTCGAAGGGGCGAGTTGCACAGGCCTAGGAAGGGGTGTTGCACCTTTTACTTGTCCAGCAGCCGTCTGGGCCGAACAT ATTCTGCAGGCGTAGCAATGTGCCCTCGACGTAATCAGCGATTACAGAGGGTACTGCGGTTTCGGCCTTGAAATTGCGGG GCTCTGCCAGCATGCCGGCGCTGGAATCCAGGCGCTCTCGGTAATTCCAGATTTTTCCTACAGGCCTAGCGAACTGCTGG GAGGCGCAGCTACCTTTCGTCCGGTAGCCGGCCCCTCAGTATCGGTATCGCTAGGCGAGACTGCTTCGGGCGGTAGATCC CCATCCTCCAGATCCGCTTGTTGCGGTGGAAGCCGCGGAGGCCGTGGCGGCACGGTTCGATAGGTGTTGAGCCATCAGAG TGAACAGCACGCTTTGCTCGAAGGTGTCAGGTGGCTGTGGTAGCGCTTCTTCCCACGCGGTTGCATCTCCCTGAATGCCT TTGCCCGCATGGCTTCGGTTTGGCAGAGGCTTGCGGGGAGCCGCTGTAATCCACCTTCCTGACGTTCTCCAGCGCTCCTT GGGCCAGGCTTCTGGCATGCAGCACGGCACGCATGTGGTCGTAGTCGGCCTCGATGTAGCTCATGGTGGTCTGGATATTC GAGTGGTTGAGCAGGCACTTCGTGAGGTGGATGTTCCGCTCGGGTGCCTTCATCAAGTCGGTGGCCAGGGTGTGCCGGAA ACGGTGCGGAGTCATCCGCACCCCAACCTTCTCGGTCAACTTCCGGTACATGGCTTCGACCTGGTCGGAGTTCATCACCT TGCTCTTGTAGTGCGGTGAGAACCGGTTGACGTTGAACAACTGGTCGTCGTCGAATCCGGCGAATCCGGCTCTATCGGCCTCCTGC GATGAGGATCAGTTGATTTTCCCAGTCGATGTCGCGCTTGCGGATGCACAACAGCGCATTCAACCGGATGCCGGTGAAGT ${\tt GGTCTTTCTGAACGGGTTGACTTGGGAGTGTCTCACCAGCTCGTGCTCGATGGCATAGCCCCAGATCGTTCGCAGATGAT}$ TCGAATACGTGTTCCAGCTCCGCTTCGACAGGCCTTGTTCCAGGACCTTGCGCCCCCCATCCCAGCACAGACCTGTGGTCC CTTGAAGATTCCTGGCGTGACCAGCATGGCGGTCCCGTCGACGGTATGCACCAAAGCCTTGGTGTCGTTGATGAACAGGC GACGGGTCGCGATACCAGATTTCATCCAGCCAATGAATCCCTGTCCCAGATCAGTGCTTCTGCTAGGCATAAATACATCT TCAATTGCTTCAGGAGCGCAATCTGTAGTGGTCAACCCATCCCGGACAGTGGGTTGAGTTTTTCTTCGGCCACCGCAGGT GGTAACCCGTCGTTGAATTGATGCGGCCTGATCCAGTTGTAGCGGTGCATCAAGTAATGACTGATGTCCCGTTGGGCCTC AGCAATTCCCCCGACGGCTCATGCTCTGCTGCATCCGATAGCGCCAGAGCCGTTGCCGAAACAGGCGGCTGGCGTACTGG CTGCCCTGGTCTGAATGGAACAGCACCTGCTGTGGCCTGCCGCGCTGTTCGTAGGCCATGTCCAGGGCCTTGATCACCAG CCCAGACGTAGGTGATGTCGCCACACCACACCTGTATGGGATGCTCGGTCGCGAATTCGCGGTTCAGCCGATTCGGGATA ACGCACTCGGAAACGGCCGATGGTCACGCCCTCTTCGCGCAGCATGCCCAGAATGCTGCGGCTGCCGGCCCGAGCCCCGAC GTACGATCGAGTTCGTCCGACATCAAGAGAGCGGTAGCCTTTTTTAATATCGCTTTCTCCCGCTCCAATCGGTTGATCCG GGCTTCCAGCTCCTGGATCTTTTGCTGCTCAGGCGTCAACGCCTTGCTCTTCCGGGGTCACACCCTGGCGCTCCGCCTCGA GCTGCTTCACCCAACGGCGCAAGGCCGAATCCACCACCCCCAGCGAACGGCAGGCGTCGATATGGCTGTAGCCTTGGTCC AGGAAGGCTGCGCTGAGATTCCTACTAGTGAATTAGATAGTTGTTGTCTTCTGAAACAGAACTGAAGCGAAATTGGGGGT AGGGTTTTTCTAGGTGAAGGGTAACTCTTGAGAATTACAAAGGTGTGACGCAAATGTTGTATTTTTCTTGCAGTATGAAG ATGGGTGGTTGGGTCGGATATAGGTACTTCTCTCTATTTTCTTTAATTGCTCTCATCTATGGGTGTCGGTGGTGGAGG TGAGGTTGAATCGGCTGAACTGCGATCCAATTGAAGGTCGTGTTCTTGAATCAGAGAAGCTGATAAGAAAGCCGCCCAAT GAGCTGGGTATTCACTGAGTTAATAATTTTTAGCCTGGAGAGGGTCTTTTTGAAAATGAAAAATCACTTGTTATGTCGGC TGTGCTTTTGGTGGCTAGCAATTTCGCGTGTGCTGATGAGGGCTCAAATGATGGAAGTGAGATATGTCGGGCGCAGGGTG GAGTTGAAATAACAAGTCTGGGGGAAGTCTCAAAGGGTGTGGATGTTGAAGATGTTGTAGTTTGTTCGATTCTTCCAAGT AATATGAAGTCGAGTCAAAGAGCGCCTACACTCCCTCCTCTGCAAAGGATGATCATTTCGGCAATGCCTTCACCAGGAAC GGTCACTGTTTCTGCCAGCGGAGATAGGAAATTTACAACATCTTGCCGGGCAAATCTTTATGCTCCACGTTATGCCAATT TCTATCCAGACGGTGTTAGCAGGGGAACATCAGATCTACGATGTGTTAGCAATACACCCGGGGAATTCATCTCAAGGG TGTAATGTGTCATGGGACGGCCCGACCGACATTCAATTGGGTGTTGAGCCATATGGCGGATCTGTTGTTAAACTACAG AGAATGTGTCAGGAATAATAAATGTGGTTTTGAACTAAGGATGCGCCTTAGTAGGATTTTATTTCAAGGTGTTCAGCTTG TGAATGTGCTGCAGGGCACTCTATAGAGTGCCCTGCATAGGCTGGAAGTCGTTTGGCTGAGGGCTAGTCTTTCGAGTTCG GAGTTCAAGGTAGGGTTCCGACGCCGAGGATCCTCTTTGGGTGGAGTCATTTGCTGAGCCATGCAGTTATAAGACAGGCT CCTGCTGTGCCAAACCAACTATAGGCAACAAGAATATAATTCGAAGAATTTTAATAAGCATTCCAATCTCCTTAACCCTG AGGGTTGGATGAGACTCAATAGTAACCTCAAGTTATGAGGAAAGATGAACCGCCTATCGTTTTGTAGTCTTGGTTAGGTC GTGCGGGCTTGTACCGGTTCGAGGAAGGAATAGACAGCAGACAGGATCGCTTGCGATGGGGCAGCAGGAAACCATCAGCC CGTCCGTATCCAGAACTGCTGCTTGCAGCGTTAGGGGTGACTCCCTCATGCCCTAGAGGGCATAATCCCTGTATGGAGAT

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FIGURE 1B

GGTGAAGTGCAGGGCATCCTGGAGGCCCAAAAGAGGGATGTTGGAATCCTCGCCGACTTCTTAGCCAAGAGTCTCGTGGC TTCGTCCTGTCTGGTTGTCCCGGATGACGAGGGTCGGGGTCGCTGTAATGCCCTTCGACTGTGCGGTGTCGATGTTCGTA AGCGTCCGGGGAAGGCACATTGCGATGCGCTAAGCTGTAATCCTTTAGGATTGAGGTCTCAGCATGGAATGCCACGTTCG TCCCGCCACGAGCAGAGATGCAGCGATAAGCTGCGTAGTTATAGCCGCCCTGCGTGAGTCAAATTCACAGGACTATC CGCCTGATGTGATCGCTCAGGTTGAGCAGAGCTTTTCTCCTGAAGCCATCACCACAGCTTACGAAGCGTAGGGTCTTC GTAGCCTTATTGGGCGAAAACATTATTGGCACTGCCGGTCTCGACGGTGACGTCGTCAGAAGTGTTTTCGTTGACCCAGC GTGTGCCATCGTCGATTACAGCTGAAAGGTTTTATACCGCATTGGGTTATCAGAAAATCCGCGACGAGTTTCATGGGGCG GAGCGCACCATCGTTATGGAGAAGCGGCTGTAGGATTATTCCAGACTATTTACCCACTTATGCGGCAACAAATCAGTGAT CTCACTGGCCCGCTGCGTGGGCAGCCGCGTCAGCACATCTTTGAGATAGGCATACGGATCATGCCCATTCATACGCGCCG ACTAGATCAGGCTCATGATTGCAGCCGCCCGTTTACCACTGCGCAGCCGGCAAACAGCCAGTTCGAACGCCCGAGC GCCCATGGCCGTATTTGGTTCTCGACCTGATTGTTATCGATGGGCACAGCCCCATCGTCCAGGTAGCGCGTCAGCGCTAC CCAGCGTTTCAGGCTGTAATCGAGGGCTTTGGCCGTGGCTGATCCATTGGGCACCAGGTCTCGCTGAGCCAACATCCAGT CATGCAGTTTTTTGAGGATCGGCACCGCCAATTCTTGTCGTATTCGCCAGCGCTCTTCATCACTCATGTCCCGCGCCTGA GAACTTGCGCCGGGCGTGGGCCATGCAGCCGATTTCAGTGATGCCTTGTTCGAAACCGGCTTTGTAGCCAGCGAAGTCGT CGCAGACCAGCTTGCCGTTCCAGTCACCCAGGAAGTTGCGCGCATGTTCGCCAGCACGGCTTGGGCTGAAGTCGTAAACC CATTTGCACCGGTGTTTCATCAGCGTGGATCACGCCCTGGTTCAGCACGGCTTCACGCAGTGCATCGACCAGTGGCTGAA TGCCGGTACAGCGGCAAGTGATCGGCAAACTTGGCCACCATCACGTGGGCCAACAAACCTGCGGTCGGGATACCTTTGTC GATTGACCTGCCCCCGATTTCAGTACCACGCTGAACTTAGTAGAATCCGTTTTCCAAGCAGGAGACGGCAGTGCAGAAG AGTATCGACGCTGTAGCTAACGCCGCCTGCACATCCTGCTGTGGCGTGCAGGTCAACCACAAGCGGATTTACCGGCTGTA ACCAAGGTGTCGGTCGACATCTTGGTGGAGTACGGTATCAGCGGTTTTCGTGTCACGCGGGCGCTGGACGAGATGGCCCG $\tt GTTTCGTGGCTACCCGCAGGCGATCCGCACCAGGGCCCCGAGTTCACCGGCAAGGCGCTTGATCAGTGGGCCTGTC$ AGCGTGACATCAAGTTGAAGCTGATTCAGCCTGGCCAGCCCACGCAGAGCCCCTTCATCGAGTCATTCAACGGCAAGTTC CGGGGCGAATGCCTCAATGAGCACTGCTCGCTGGTCGAAGCCAGAATCCGTATCGCGGCTTGGCGGGATTACAACGAGCA GGGAAAAGTTGATATCAACCCCATAGCCTACTAACTAGGCAGCGGTACTAAAACTGGGGGCCAGGCCAGTCCGAACTGATA AAAAAACGTCCGAAACTGGCAAAACCTTATGGCCGGTTTTCCTAATATTTGCTCCGAACCCTCGGTATTTCAAGGAGCGA CAGGGCCGCGGCAGATCACTCTGCGCCAGTTTGAGAACGGAGTCACCGAGCTACAGCTCAGTCGGCCACCATTGACCAGT TCAAGACCCTTTCCGACAAGATGGATCTTATTTCGCTGCTCGACAGCTCGAACAAGAAGCTGAAGCTGTTCCAACACATT AGCAGCGAGATCGCCGCATCGCTGAAAAAGGGCTTGGGCAACAAGATCGGCGGCTTCTCTGAGTTGCTCCAATGTACT $\verb|CCCACGCATAGATCGCGGGCTGAGCCCCTAGAACGCCTATTGCGCGACGAGACACGCAAGGCCGTGCTCGGACAGATCG|\\$ $\tt CTACGCATCCAGAGGTTGCACCCAGCCGACCGTTGCCGCCAGCAGATTGCAGTCCGGCTCCGGAGTCACCTTT$ CAGGAGTGTTCCAGAAGGTCAGCTTGAGTGATCAGCCGTACCAGGCCGGCGTAGAGTGGACAGAATTCCAGGATGGCGGG GGGTGCCTGCCGCGCGCGCGAAATGCTGCAGCTCGAGGGCCTGGAGGAATTGCGCGAGCAAACCGTTGTGGTGCCG TTGAAGAGCGAGCGCGTGATTTCAGTGGCATGCTCGGTGGCACCTTGAACTTCACCATGCCGGACGAGATCAAGGCGCAC TCTTCAGGAGCGCCTCCAGGAGCGAGTCGGTGAACATCTGGAGAAACGTCTTCAGGCCTTCAGAGCGTCATACCTTCGCTT GCGGTGGCTTTTCGCCAGAAGGCGCGGGATGCGTTCACCGAGCTGACTGTCGCTATCGTTAGCGCCAATGGCTTGGCGGG ${\tt TAGGCTCAAGTTGGACGAGGCTATGCGCTCCGCTCTTCAGCGACTCGATGCGCTGGCAGATACTCCGGAACGCCTAGCAT}$ ATGCCACCAGTCCGGCGGAAATCAATCAAGCGCTGAACGATATCGTCGACAACTACTCGGCACGAGGCTTCCTGCGTTTC GCACAGTGGGGCTTGAGACTTCCCTCGAGCAACGATGCCACGTTGCGGCTGCAACCGGCAGAGGGACCGGAACTGGTTAT GGAGCGCCTCGAGGGCGGTTGGCTTTTCGTCGTCGAGTTGGGACTTGTGCCTTCAGGGTTACCGCTGGGTGTGATCTTGC ${\tt AATTGTTACAAGTGAACTCTCCATTCTCATCCTTGGCACCGGTGAAACTTGCGGCGGACGATGCCGGTAGACTTGTGCTC}$ TGGGCTGAGGCACGTGATGGCGTTGACGATGTGGATGCACTGAACCGCTTGCACGATAGGCTGCGGGAAGGACATTCACG AAGGGGAAGGACCATACTGCCAATAAAATCCGCAGTTGGTAATTTCTCTAATAGATGGGCCACCCGAAGGTGGCCTATC TGTTCATGCTGCAATGAGTTGTCGTGCCAACACCATTTCTACCGAGCCCCATCCTGGTTCAACGAGCCGAGGCCCTCGAG TTATATCGGCACTGGCCCACATTCGTGTGCCTGCCAGTCTGTTTCCAT

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FIGURE 2A

The Big Island: 84830bp (SEQ ID NO: 2)

CACCGGCGATGCATGGGATGCCGTAGGGGTCGCTGATCCAGCCGAGGCCGCCCTGGATGGTTTTCTGGTCGGCGCTGGCG GAACGTGAGGCTGCGGATCTGCCCACGCACGCAGGAGAGTGTCCAGTCGCCCGAGGCGGTCCCGCTGGCTACCGCGCCGG GTCCCGTCGACCGGCACACGACCGATCAGCGCAAACATGGCCCACCGAGCCCATGAGCGTCGAGTTCTGCGGCAGCGTGTA GGTCTTACGGACGAGCTTGCCGGTTTTCCAGGTCAGATCGCTGTTGGCCGACGGGGTGCAGCCCGTCATCGATCCGCTCCA GCCAGCGGCTGGCCATTGGCATCAACCGCGGGGCGTCCTGGGGCTCGATCCAGACGATATCCGATGAAGACGAGCCCGC TCCCTGAAAGTGCTGGCCATCCTTTGGTCGCACGCCGAATCCTACGGGCAGGTCGGTGTCACCGGCCTCGGGAATGTGGG TTAGGTTCTCGAGCCGTTTCTGTACCTGGTCCAGGATCGTCTGGCTACGGTTTTCCTGCTGTTGCTGCAGTTCCTGGGCG GTGTTGTTGAGCTTCTGCTCGATGTTCTGATCGATGTTGCGCAGGCCGCCCTGCAGGTTCTCATTGGCGGCTTTGAGCGA GTCATTCTCCTGGATCACCTTGCTGATCTGGTCCTTGAGCTGCCGGCTTTCCGCCACGATGGTGCGTAGTGTCGGCGG GCGTGTCGCCGTCGATGCCCAGGGTTGCCGCTTCTTCCGACGTTACCGTCGGGGTTGCGGCGCCTTGTGACTGCGCACTT TCTTTCTTGCCCATCATGCTCACGCCGATCAGGATGGCGCCGATCACGACGGGGACGACCAGCAATTTCAGGAGGGGATT CCGCGCGTCACCAGATACACGGTAGTGGTGTCGGAGGCGTCGCCCCGGGGCCCCAAGTACGGGTGCTGGAAGGTCGCGGC GACGAAATTGCCCATCAGGTCCCTGGGATCCAGGGCCAGGTGCTGGCGCTTGGCGGCTTCTGCAGCTTCACCGCCGTGATGT AGTAGTCGTCCAGCCGCCAGGCGCCCAAGGCGGTAGCCGTGATGGGTAGGCTGGGGAGCAGGGTGGTCAGGTCGAGCTGT CGCTTGACGCGCACCCGACGCCATCCACCGGTTCCACCGTGCGAAGCGGGGCATAGAGCATCTGCGCCGCATAGCG ATGGCTGGGCTTCCCGGGACTGGCCATAATGCGGATCCACTGGCTCGCCGGCGACGATCCTGACCGGCTCGCGCGGCTGT TGGTCGGCCGTTGCTTCGGTGGCGGCGATATCGATGAGCATCTGCTCGCCATTGGTCGCGTCCTGTAGGCGCAGGCGCGC TGGAGGAATCGGCTCGTTGGCGAGCAGGTAGAGTGCGCCGCCGGTACTCTGGACGCGCAGCTTGCCCTGCAGATCCCGAG GAACCCCAACTCGCACGTTTCTGTCGACGAAAACAATGCGTTCCTGGCCGACCGTCAATGGAATGGCCAACGGAATGCGC ${\tt CATAGACCTCCCTCCCGCTTGGTGGGGGGCGGCCGGCTCCTCAAGCTCGATACGTTGAGGCGTGTCGGAGTAGCAGTCCCA}$ CTGCAGGCCGAAGGGATTGGTTTCCGGGTCGACGTCGGCGGGGATAACGTGCAACGGGTAGCGGCCCAGCCCCGCTTGA CCACCTCGCCGTCCTTGGGCCAACGCTGCACCTGCTGGAAGATGTAGAGGCCGAACGCATAGACGCTCTCTGGCGGAATG ATGGGAAGGCCCTTACATGATGGCGGTGGCTTTGGTGACGAGATAAATGATCAAGATCAGCAGGCCGACACCTACGGCTA AGAAAGACAGCCGCGCAGATGAGCAGCGCGAGGAGCATCGCTCCGTCATAGCCGAAGTTCTGGATGGTTTGCATGATGCC CGATCCCTCCCCACGGCTAGGTGCCTCGGGTTTGGGGAGTGCAGCCAAAGGCGATACCGGGGAGCGCCAAAGTGATGGCGG CCAGGCTCTGGCAGAGGGCGGACAGTTTCTGGAGGGTGAGTTTCAGCATGAGTGTCTCCGTATGGGTCAGCTGAGGAGGA AGAAAGAGGTGATGCCGAGGAGGACCAAGATCCGGGATCGCGGAAGCGCCACCGGTGGCGCTGTCGAAGGTTGTTGGTGG TCGCCGGCCGATGGGGGAAAGCCAGCGGCGGCCTGGAACGCTGATGTCTGGGCTCCATGCTCATGGCATCGGCCCT TTGGCGGATGCGCTGCAGGTCAGCGGCCAGGCGCGGGTAGTCGAAGTAGAAGCGCTGTCCGGGCTCATCGGCGCCCTGGG CACGGCGAATCTCGTGCAGATCAGGGTGCGATCAGCTTGCCGATCGCCCTGATTCCATTCCGCAAGAAATACTCGGCGCG CCTTGGGCGTTTTGATTACCGATCTCGGTTACGCCCCGCATGAGTGGCTGAACGCTCACCAGCTCCCAGCCTTCCTGGCC ${\tt ACATCGCGACGCCCTTGGTGAGGGTTTTGTAGGGAATGACGATGTTCTCGACATGGTATTCGAAGGGCTGTTTTATGCTC}$ ATGGTGTGCTCCTGGATCGGTTCGAGTAGAACCGCACGGTTTCAAGAGCAGGAGGAGGGCCTCAACCGAAAATACTAGGC $\tt CTAGCACCAGTGAATTTCTGGTGGTTGGCGGGTTTAGAGACACGTATGGACGTCTGGGTGTATATTTCATATATTTCT$ AAGGGAGACGGCTGATGCTTAGAAACATCTCTATTGGAGTTTTGCTAGCCATGGCTGCTATGTTGGGCAGTTATGGGGTG CCCTGATAGCCGTAAAATTGAAGGGCCCGCAGTGGATGGTAGTGGCTATATAGTGCGGGGGGCTGCTACTGTCGAAAACT GGGTATATGGACCAAGGAATGGATGGTACCAGAAGCTTAGGTTTGTCGATGGAAGACTAGTTCAGATAAAAGGCAGTATG GACTAGGGTATAGCCGTGGATGGTGTTTTCATCCACGGCTATAAGTCTCATCCGGCAGATGATATAAGGGTAAGGATA TTTGCGATTGGTAGGCCTTGTGCGTCGGAAATAAACACGGTTGTACTGGCGCCTGCACGGGAAAACTATCTGTTGTAGGT GTTTGAAGTGAGTTGGGCACCATTAAAGTTGGCGCTGAATTTTTTAGTGTTGCCCGCGATGTTGATGGCCTGTAAAAGGG

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GCTTATATTAACCGCCTGTGCGGTATTGACGCTAATGGATGTTCGGGTTCCTGCGGCGTCTAAAGCTTGTTGAATGTTGT TTGAAGTAAGTTGAGCGCCATTGAACTCTGCGCTGAATGTTTTTGTGTCACCTGCTGCATGAATAGTTTGAAGAAGGGCG GTTATATTTGCCGCTTGTGCGGTATTGACGCTTATGCTGGTGTTTTGTTCCTGCCGCATTTACTGCTCTAAGTAGGTTGTC GCTGCTGAGTTGGGCTCCATTGAATTCTGCGCTAAAATTCTTTGAGTTGCCTGCTGTAGATATTGCGGAAAGAAGTGTGT TTATATTAATGGCTTGTGCGGCTATTGTGGATACTCTGGTTAGTGATCCTGCTGAGTTTATGACTTGCTGAAGGTTGTTA GATTTAGAAGGCGTCCGTCGAAATCAAGGATAAGTTTCATCTCAATGCTCCGCTGTGACCTAACGTTAAAGTCTTGGTGT GAGTACTTCCTAGGCTGAATGAGTTGGCTACAAATCTCTTTGCCTTATGTCAATATCAGGCATTCGCTGTGACCAATATC AGATCAGGGTAGGTCGATATGATCTTGATCGAGCGAAGCATCTCACCGTCCTGGCTGATCTCGGCGATCTCCACGTACTG ${\tt GGTGTAGTCGCGGTAGTCACGGAGCAGTTTCTTGTTCTGGACGTTTTGGCGCAGGCCTCGGCTGAATGCGTACAGATCCT}$ GGCCGAATCGCCAGCTCTGGGTCAGGTAGTGCTCCTCGGCCGCCATCCAGTCGCTGTTCAGGGCATCTTCTGCGCCC TGGGTTGATGTCCTGCCCCTCGTCCAGGAGCATGCAGTCGAAGCGCTGGCTCAAATCGGGCTTGCTCAGTTGATACAGCT ${\tt TGGGCGGTCTTGCACACTACGTTGCGGGGAAACTTGCCCTTCGCGGCTTTCTCCACCGAGCTGTTGTAGCAGAGATAGAG$ GATTCTCAGGGTAGGGTTCGACCTGGCAAAGCCCACCAGGGTGGTAGTTTTGCCAGTGCCTGCGAAGGCTCGCACCAGGA TCTTCGGTGCCTTCGACTGGATGATCGGTGACTGTTCGTGAGTCCACTGCACGGCGGGTCTCCTACAGGTACTTTTTGAA TCCCGGCCGGCGCCGAACTTGCGCAGGTCCCGGCGCACCAGGCCGTCCACCAGGCCGGTGAACGCGGCCATCACGAATAA GCGTGGAGACACCGTGGGCGGTGAGATAGCGAACGTCCAGCGGGCTCCGTGGCCGGGCCTGCGCGATGGTAGTCATGTTG ATTCAGGAGCAGGAGTAGGGGGGCAATCGAAAATGCCAAGACTGGTGCCGTGGGTTTTCTGGGGTAGCCGCGGGAGAATG ${\tt AACAAAGATGTTCAAACGTTCCTATAGGAAACTGTGTTGTGAACTCCATAGAACTCCCCTTTTACACGATGCAGGTTGTT}$ ${\tt TGAATAGCGCTGTGCCTGCAGTCCTGAGACCTCATTAGGAATCATCTGATAGAGGGAATTTTTCCATGCCGTCAGTCTTT}$ $\tt CTCAGTCGGCAAGCTATGAATGTGCGAAGCGCAGCTTTATTTCGAGCAGCGCGAGGCGTTGCTCAATCACTT$ GAGCGGCAATGTCGTGCCCTTGGCCGCGGGTAGAGCGCTCGTCAACGAAGCGCCGAACAATGTGAGCATCCTGCCGTTGA $\tt GTGACGGAGGCGAGGTCTGCTATTGACCGCTCGCACGCTCGGTGATCTCCGGGAAAAGCGGCTGGCACTGATGTATCTG$ GTCGATACCGACAAAGGCCCTCTGGTTTACCGGCTTACCGCCGATGGTAGGCCCTCGGCAGCGATATCCAGCACGATAAC GCTGGGGAGCGTGCGTCGCGGACGCTTTTGCGTGGAGACGGCTTCGGTTTCATCGGTGCTGGCCCACTGCCGCAGCATA ACGCTTGATAGAGCCCGCAAAGCGACGCCTTGAAGCATTGAAGGAGAGCGAAGCCTTTTCCCGTGCAGTTATCCAGGCCG CGCCCGTCGCGCTGTGCGTGCGTCGTGCCGACGCCGCAGTGGTCCTGGAAAATCCCCAGGCGCCCAATGGCTGGGT GATAGCGAGGCGATTGCCCACGACGCGCGAGATGGATTTCCCAGGCGTTCGCAGGAGGTGTGAAGTGTTCTGGAGAAGA ${\tt ACTGGAAACCGAGGCCTACATCTTCATCTCAATTACACGCCCACCCGCTATAACGGTGAAGACGTATTGTTCTGCG}$ ${\tt TCAGCGATGTGCTTGACGTATCCAAGATAGAGGCCGGCCAACTGGACCTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACCTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTGGACTAGAGTGCGTGGAATTCTCCCCGCTGGAATTGGACTGGACTGGACTGGAATTCTCCCCGCTGGAATTGGACTGGACTGGAATTCTCCCCGCTGGAATTGGACTGGACTGGACTGGAATTCTCCCCGCTGGAATTGGACTGGACTGGAATTGA$ $. \ A CAATGGCTATGTCAACGTCCACCTGAAGGCCAGCGTGGTCGATGCCGAATGTGTGATGCTGACCTGGCAGGTCAACGAT$ ACCGGCATGGGGATCAACGTCGAGGATCAGCCGCGTCTGTTCGAACCGTTCTACCAGATACGCCGCTCCGAGCATCCGGT CGATGTTCGAAGCATGGCCAGGATGCCGGGTGGAGCTTTCCCCTCAGGGTGATATGGAGCCGCAGGCACAGGGCCGCGAC

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FIGURE 2C

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TGGCTGCTCGGGCTCAACAACCTGAACGGCCTGCATCGTGCTCTGGGCCTGGCCCCATGGGCGTCTCGCTGATCCTTCGAC GCCGCCGATACGGCTGGCTCCGTTGCGCAATCTAGGTCTCCGCGTCCTAGTGGTGGAGGATAACGCGATCAACCAGTTGA TCTTGAGGGACCAGATGGAAGCGCTGGGCTGCAGCGTGGAGCTCTTCGATGGTCGCGAGGCGTTGCTGCCAG ACGGCCTGCTTCGACGTGGTGCTCACCGATATCAACATGCCGAACATGAACGGATACGAGCTAACCGCGGAGCTACGGCG CCAAGGGTTCCGGCAGCCGATCATCGGCGCGACGGTGAACGCCATGCGTGAGGAGCGCGAGCGCTGCATGTCCGCCGGGA TGAACGATTGCCTGGTCAAACCGGTGGATCTGAATGCCCTTCAGAACTGCTTGATTAATATTCTCAAGGTGGATCGATGA GCTGGAAATCCTATCGGGTGCTGGTGGTCGAAGATCAGCCGTTTCAGCGCGAATACCTGCTCAACCTGTTTCGCGAGCGC GGCGTGCAGTACCTGGTAGGTGCCGGCGACGGCGCGGAGGCGTTGCGCTGACCTGAAGCAGGACAGGTTCGACCTGATCCT CAGCGATCTGATGATGCCGGGCATGGATGGTATCCAAATGATCCTGCAACTGCCGTATCTCAAGCATCGTCCGAAGCTGG CGCTGATGAGCTCCTCGTCGCAGCGGATGATGCTCAGTGCCAGCCGGGTCGCCCAGAGTCTCGGCTTGTCGGTAATCGAC CTGTTGCCCAAGCCGACTCTGCCCAAGGCCATCGGCCAACTTCTGGAACACCTGGAAAGATGCCTCAGGCAGAAGCTGGA GCCGGAAACCGACGAGACTCCGCATGGGCGCACGGCGTTGCTGGATGCCCTGCATAACGAGCAACTGGTGACCTGGTTCC AGGCTAAGAAATCCCTCCACACCGGGCGCATAGTCGGCGCCGAGGCGTTGATACGCTGGAGCCACCCGCAGCATGGCCTG TTGCTGCCCAGCTGTTTCATGAGTGATGTCGACGCTACCGGTCTGCACGAGGCGTTGCTCTGGCGCGTGCTCGAACAGAC CCTGAACGCCCAGGAATCGTGGCGCAGGGCGGGTTACGAGATTCCGGTTTCGGTGAATCTGCCGCCGCACCTGCTCGATA ACCAGGAACTTCCGGATCGACTCTATGAGTACGTCGGCGCGCTCGCGGGGCTTGTACCAGCTCACTATGTTTCGAGTTGACC GAGAGCAGTGTCACAACTCTGTCAAGTAACTACTATGCAGGTGCCTGTCGCTTGCGCATGAAAGGGTTCGGATTGGCCCA GGACGACTTTGGCCAGGGTTACAGCTCGTTCTATAACCTGGTCACGACGCCTTTCACGGAGCTGAAGATCGACCGCTCCC TAGTCCAGGGATGCGTAGAGGATAACGGCCTCAATGCAGCTGTCATCAGTTGTATTGAGTTGGGTCACCGCCTGAATCTC GACGTGGTGGCCGAAGGCGTGGAGACCTGCGAGGAACTGAATCTTCTTCGTCGTCTTTGGCTGCGACCGGGCGCAGGGTTT CCTGATTTCTAAGGCAGTGTCTGCTCGTGAGTTCGAGCGGCAGTTAAGGGAGGACGGCCCCAGCCTCCTTGTTTAACGCA -GTATCCCCATTATCGCGGAGTCGATCGCAGCCAĀČČACCGŤCAGCGCAACAĞTGTCGCTGAAGGAGGCCGCATCCCGTGA AGTCTGCTAGTGCCTTGGAGCACGACAACAAACTTTTGCTCAAATGGACAACCCTCTCGCAGAGCCTGAGCATCGGCTTG ATCTGTGTGGTGGTGCTGACCGTATTGCTGTTCAGCATCTGTTACTGGTCGCTGGGGAGATTGTTTCAGGAGGAGGAGGAGGA ${\tt CAAAGTCTCCTTCCACCTCGCTATGATGGATGTTATACGGGAGCATGAGGTATTTCTTGGGCGCATCGCTCGAAAAA}$ ${\tt GCGACAAGACCACCCAGAAGTACGACTATGACGTGGTGCCTTTGCAGCGGCACTTGTTGGCAAAGGAAAACGGATTAGCG}$ $\tt GTCTATGAGGGACGGGAGTTTTCCTTTGCTATGCCATTTCTACTGGCTACCAAGCACGCGTTGAGCGCCGATTCCTCGGG$ A GATCCGTTTTCGCTCGGTGTATTGCTCGCCAATTTCTACGGAAGCTTCTGGAGTGTTTCCGCCTATCCCGCCCACAGTTACTGATCTTTGATCTTTCCGGCAGCACCCGCCTGGCAGTGCCGTCGATTCCCTCCACAGCGCAGCGTGACAGGTTGAGC $\tt TTGGATACGCGCTGATCGCGACTCGGCGCTGGAGATGTTGGGAGTCGCCCGGGTTGATCTGCCGGAAACACTCT$ GGTGGCACGACGAGCCGAACCATCTGATCATCGCTGCGAGCCTGCTTGATCTCAGGCGAATCAATGACTTCGAACAGTTG $\tt GTTGAGCGCCCGGCATTCGATTCGTACAGCCTGGTATCGCCGGATGGCGAGGTATTGCTCGGCGCGCCCCTGCGACCGG$ $\tt CTGGCCGGTTGGCTCGGGATGCGTTGGTACACCAGCAGCGTCGTCAACCCGGTGCATCGGGCGCAACTGGTGGA$ TGACCTGCAACCACTTGGCCGCCCAGTGGCTGGGCGGGCCCACGGAGATCCTTGGGCTGACTTCCAACTGGAAGCTTTTC ${\tt GATGCGCGTGGGCAGGTACCAGGAGACATCTGTATCCAGGTCGGTGGGCGCTATTTGCAGACCGCCTTCGCGGCGACCCG}$ $\tt CGAAGCGAGCAGCCAGCCAGGCCAAGACCCTGTTCCTGGCCCGCATGAGCCATGAAATCCGTACTCCCCTG$ GAGTTCGTCTGCGACGCTCATGCAACTGATTAGCGATGTGCTGGATGTCTCGAAGATCGAAGCGGGGCAGATGGCTCTGA $\tt CCCTGGCCGCCTTCAATCCGCTGGACCTAGTGCGGGAAGTGCTTGGCCAACTTTGCCGCCAGCGCCATGGCCAAGGACCTG$ CAGTTCTATGCCTGCATCGACACCGAAGTGCCGGCGCAACTGATCGGTGACGTGACGCGGATTCGCCAGGTGCTCAATAA $\tt CTTGGTGAATAACGCGCTGAAGTTCACCGATATCGGACGGGTGGTCCTGCGCGTGAAGTTGCTCTCCCGCAATGATGGTC$ GAGCCCTGTTGCAGTGGCAGGTCGCCGACACCGGTATCGGTATCGCACACGAACAGCAGGAGCGCTTGTTCGAGGCGGTTC TACCAGGTTTCGGGAGCGCACCATGCCGGCGCACGGGGCTAGGACTGTCGATCTGCTGGCATCTGGCGGAAATGATGGG $\tt CGGTCACCTGCGAATGGTCAGCGAGACAGGGTCGGCAGCAGCTTCAGCCTGGTGCTCGAGTTGCCCGAGGACGAACAGT$ GTAGGGGCGTGGCTGAAAGCCTGGGGCTGCAAGGTCAGCAGCGGCGAGGCGGCGCCCCCCCGAGCTGGAGACTTGTGTGCT TCTGGAGCTGCTGCCGATGGCGGCCCGGGCCTGCTTCTTCGCCCTGGCCAGGCCCCCGGGTGCGCGCCCCATGGATGCGC GCTCTGGGTGGCGATATCCCCGAGCAAACGCCGGCAAATGCCTGCGCCCGCTCGGGGAGACTCGACCTGGAAGTGCTGGT ATGGGCGGCAGGCCCTGCAGCTGTTCGACAGTGGTCGCTTCGACCTCCTGCTCAGCGACGTCAACATGCCGAACATGACC GGCTACGAACTGACCCAGGCGCTGCGCGAACGAGGCGAGACGCTGCCGATCATCGGCGTGACCGCCAACGCCCTGCGAGA AGAGGGCGAGCGCTGCCGGGCAGTGGGAATGAACAGTTGGCTGGTGAAGCCGATCACTCTGCATACCTTGCATGAACTGC CTCTCACCGCAGGTGCCGGAACGCATGCGCGCGCTTTTCCTTGAGACCATGGGCAAGGACCTGGAGGCCGCCCGGCAAGC $\tt CGCTGGTGGTGATGTCAGGGCGCCGAGGAAGGCCTGCTGGAGTCGCGCCTTGAATGTTCCGCCGTGGAGATTGGCAGATTGGCGAGATTGGCGAGATTGGCGAGATTGGCGAGATTGGCGAGATTGGAGATTGGCGAGATTGGCAGATTGGAGAATTGGAGATTGGAGAATTGGAAATGAAT$ GTGCTCGTTCATATCGAGCAGCCGCTGGAGTTTGTGAGAAAGACGGGCTGATGCGTCCGGGGTCAATAGTTGGAATTAGA ACACAAGAGAAGCCTATGAGTAAGCTCAAGATAGTACTGGCCGATGACCATCCGATCGTGCGTATGGGCGTATGCGACAT GCTCGAGCGCGACGGTCGGTTCGAGGTGGTGGGCGAGGCCTCCACGCCCAGCGAACTGGTCGAGGTGTGCCGGCAGAGCG AGCCGCATATCGCCATTACCGACTACAGCATGCCCGGGGACGAGCGCTACGGCGATGGACTGAAACTGATCGACTACCTG TTGCGCAACTTTCCTCGTACTAAGGTGCTCATCTTCACCATGGTCGGCAACCGCCTGATCCTCGACAGCCTCTACGATCA CGGGGTGTCCGGCGTGGTGCTGAAGAGCGGCGAACTCGACGAGCTGCTCTTGGCGCTCGACGTGGTGAAGCAGAACCGCG TCTACCGGGGCGCGAACATGCTCGACCCGACCAGTGTTCTGGCGAACCGCGACGAAGTGGAAAGCCGCTTCGCGCGCTTG CGTCAAGACCGTAAGCACGCAGAAGGTCTCGGCGATGCGCAAGCTGGAAGTGAACAGCGACCAGGCCTTGATGACCTTCT

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GCGTGCATGCCAACTTGTTCCATTGACAAGTTTCCACCGCGGAGCGTTCGAGACGCCGCCGGCGGATGTCTCAGTGAAGCA GGCTCCGTCCTGGAGATTGCCGCCGTCATCGATCCAGCTGAAGCGCACCTCGGCCTGGCCGCCGGGCAGCGCCTGG CGGAGCGCCAGGACGCCCTGGAGAAGGGGGGCAACAGTTCGGCCGCCAGGCGGGTGTGGCCGCCAAGCTCGGCGCC GGCGAGGCTGATGAAATAGGGAGTAGGGTTCTCCATCTGTAGTGTTTCGCCCCGCCGCTCGAACCTGAGCTGGTGTGGCG CTTCTTCCGCACCTCTGGCCAGAGGGCGAGGGCGGTAGATGACTTTCATCTGGGTGCGCAGTGTAACGGTCAGCCGTGAC CAGCGCCTGGCCGGTCCGCAGCAGGCGCAGGCTGCGTTGCTGTCCGGGTTCGAGGCGGAACACCGGCGGTAGCGGCATGA TCGGCGCGCGGGCAGACTGCGGTGTCGAGTTCGGGGCGCCATCGTCGATCCAGGTCTGCACTATGACCGGATAGGCATTC TGGTTGACCAGCAGCAGCGACGTCTCGCGGTGCCCCTCGGCGATTATTGCCCGAGTGCGCTCGGCGGTGACTCCGGCTCG GGCGTCCAGCACGGCCAGCATTGCTAGGCCGAGCAGTGCCCCTTGCAGCAGGATCTTACTGGACACGAATCACTACCTGC ${\tt GCGCTGGCCTCCACCCGTCCCGGGGTAACGCTGGGCATGCTGCCAACGGTGAGTTTTTCCAGGCGCGCACGGAAGGTCTC}$ ${\tt GCTGTACTGGCTGATGCCTCCCGGTTCGCCAGTCTTGTTCGAGGCGTTGCCGATCACTGGATACCAGCCCCGTGTTTCGG}$ ${\tt CATTGCTGCCCATCGCGGAATCCTCGCTTACCAGCAGGTTCATCGCACTGCCGTCGCGCAGCAAGCGGATACCCACGCCT}$ ${\tt GGACGCGGCCTGGAGCCCTGATACCCAGTGCAGTACCGCTGGAGGCGGTGCTGTTGATCACTCCCGTTT}$ GGCACTTGAAGGCCACCTCGAAGGGCATCTCACGGTTCGCGCCGGCATTAATCTCACTGAGGGAAATCGACGGGAACACA ACGTGGGCGTGACGTTGGTTACGGAACAGGTGGGATAGCGCTTGAGCGTCACGTCGTTGTACAGGCCGATGGCGCCCGG -AGGCGGTGCGATAGGCGGACTGCAGGCCAATCGAGTTGCCCGCACTGTCGCCTCCTAGGTACCAGCCGCTGTAGAGATCG ${\tt GCTGTCGCCGTATTGGCTGAGCGGCGCCACCGAGCTGGCGATCAAGCTACCGTCGGGCTGGAAGCTGGCGTCGCTGACGT}$ TGATCACGCTCGGTAGACCGAGGGAACCGTTGCAGGTATCGCAGGCTCCGGCCCAGGTGCCGGCAGAGCCTTCACCGGGA GATCACCGCCTGTCCGGGTTCGATAGCCTGGCGAGGGCCAGTGTCGAGGTCGTAATCCAGCAGACAGGCGTCCCCTGGGC $\tt ATGTTCACACCCTGGCTGTCGAGCACATTGGCCCCTAGCGGTAGCGCGTGCCGTCGGCGAGTTGGGCCTGGATTAGCAA$ ${\tt TAGCCATTGCCGTTGACGCGCGCCCTGACCACCGCGTACGCCAGCTCCGCTGGCGCCCTTGGCCTCGACCAGGGCGAA}$ ${\tt TCGTAGTCGTCGAGATCGCGGTACCAGGTGGTCTGCTGGCGCGAATAGGCGAGGTTGTAGCTGAGCTGGCGCCAAGT}$ GTTGCTGTAGCCGAACTGCAACTGGGTGTCGCGGCTCTTGCCGTCGTAGTAGTCGCTGGTGGCTCCGGACAGATACAGGT GGTGAGAGTGGTCTGGGTCGGCTGGAAGGTCCGGCTGTAGTTCAGACCGACACGCCAGCCCTGCTTGCGCTGGCCGTTCT AGATAGTCCTCGGCCAGGCGGAGCCGAGGTTGGCGGTTAGCGAGTTGGTCAGGCCGCGCTGATAGGTGAAGTCGCCGAAGAACCGCGGAAAAGGGCACGGAAAAGCGCGAGACGCTGCCGTCGGCCTCAATCACTTGGACATCCAGATCGCCGTCGTAG ${\tt GCGGTGCCATAGAGGTCGTTGATGACGAAGGGACCGGGAGCGACGGCGGATTCGTGGACCTTCTTGCCGTTCTGGCTGAT}$ GACCACCCGTGCGTTGCTGTTCGCTGTACCGCGTACCTGTGGAGCATAGCGGCGTTGCGAGTCTGCCAGCATGCGGTCGT $\tt CGCTGGCCAGGCGCACGCCGATAACCCAGGCTGCCGAACAGATTGCCCTCGGTGAAGCTCTCGCCCAGGGTCAGTTCAGTTCGCCCAGGGTCAGTTC$ GTAGCTGTAGTTGGACTGGTGGCGCAGGCCGCACAGGCCGAAATTGATGCCCCCGCTCAGCCCCAGGTAGCCATAGTCCG AGTCGCCGTTGCCGCCTACTCCGTCGAAGCTCGAGCGATAGAAGCTGGCGTCGTAGTTGACGAAGCCCATGCTACTGCCA GCGTCCCACTCGTCGGGACCCACGTAGCCGCGTGGCTTGATATCCAGCAGGGCCTGGGGCACCGAGAGATCGAGGCGCAG AAGGGCGGTGTCGAGATTGAAGGTCGAGCCTGGCAGGCGTTCTTCCAGGCCCCAGGCAATCTCCAGGCGCTTGCACGCCGG CCTCAGAGGCGGGGCGGACGCCCAGCGTCCGGCGCAAGAAGCGTTCGCCGAAGCAGGGTTTGACGCCGCCGGGCCCGGGGG GGCCCGGTTGAAGCGTTCTAGGGTCCCGCCGGCGAGGCCCGAGCCCATCAACAGGCTGTCGAAACGATACTGCGCCT CTCCATTGGCCAGGCCCGCGAAGGCCAGCGCTAGGCCGCCCAGAGCCAGCGGCAGTTTGCCGGTGCGCCGTGCCTCAACG TGGCAGAACATGCTGGACCTCCATTCGCGCGCCGTAGTCATTGATCAAGAGGGCGTTCAACTGGACCGGTCCTGGGGCGA GCGGCGAAGGGCGTTCCGCCCACTCGGCCTGGCCTTTGGGCGGGACCATGCTCGACAGCAGCCGCCAGCGACGTTCG CCGATGCTCAGCATCGCCGCCGAAGGAGGCGTAGTAGCCGCTGGGGTTGTCCACCCGCACACGCCAGTTGCCGCTCGC GTCGACTGCGCTGCATCAGCAGCATCTGGTTGCGCTCGGCCTTGGCCAGGTCGCGGGGCGGGATCTGCAGCACATTGAGA TGGAACAACGATTCGCGATCCTCGGGCAGCGGGAGCCCGGTATACAGGAGGCGCAGGGTCTGGCCGCGGGGCTAT GCGCGTCACCGCTGGGCTGACCAGAAAGGGCGCGTTTGCAGTCTCCGGGGTGGAGGAGGGGGTCGTCGTTGTCGATCCAGG CTTGGATCACGTTGGGGAATGCGTCCTGATTGATCATCTGCACGGTCTTTTCCCGGGCGTCGCCGGGATAAATCACGCGA GTACCGATGATCACCACGCTGCTTTGAGCCGGGATGGCGGGTATCAGCAGGGCGAGCGCCAGCGTAGCCGCACGGAGCGG GAGGGCGCCGCTGGGCGCCCTCCGCTATTACTCGTAACGCAGGGTGTAGGTCACCGAGCCGAGCACCGGTCCCGGAGT GACGGTGGTCGCTTCGGAGATGTAGCGGACGGCATAGTCGTAGCTGGTGTCGCCTCCTGCGAGCACGATGTCAC

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FIGURE 2E

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GGCATCGGCCGCCGGAGCGGCGAACCGGTCAGTTGCAGGGTGAAGCTGGTTTCCCCGGCGGGTTTGCCGACTGCGCCGT GTCACTTCTCCGTGGAAGGTGATGGTATTGGCAGCCGCCGCGATACCCGGCAATGCGAGAAATGCGGCGATAGTCAGGGC ${\tt AGTACTTTGAGGTTTCATTTCAGGGTTCTCCTTGTTGAGTTTTTTCCTCCGAGCAATGGTCTGTTAAGAGCTATCCGGGC}$ $\tt GTATTTAGGACGTTTCTTAAAGGACCGAAAGTGGGTTTCTCGCTCTCGGCAAATGTTTTTACTGCAATGGACTACCCCTG$ CGGGTTCGGGTGTAGAAGACCTCGATGTAGTCAAAAACATCCGCCCGGGCCATGTCTCGGGTTTTGTAGATGCGTTTGCG GATACGCTCTTTCTTCAAACTACTGAAGAAGGATTCCGCCACGGCATATCCCAACAATTGCCGCGCCGGCTCATGCTGGG $\tt CTCCAGGTTGTTGGCAGCACAGAAGCGCTTCCAGTCGTCACTACCGTGCGGACTCCTATAGGTACTTTTTGAAGGTGGAT$ GCTGTGATGCACACCGCTACGCCGAGCAGTGCGGCGCAGGGCAACAGGATGAGCAGGGGATTGATGTTGATGGGAATTGC GTCATGACCAGGATCACCAGGCGCACGACGATGTCAGCACCGTGTACAGCGCGGCCAGGCCGTAGTTCTGCAGCGTGGA GACACCCTGGGCGGTGAGATAGCGAACGTCCAGCGGGCTCCGTGGCCCGGCCTGCGCGATGGTAGTCATGTTGGTCATCC ACGACGACGCTGTGTAGCAGCCCTGCGACAGCCAACTGAGTTCGTACTCAAACATGGCCTGGGCATGCTTCCAGCCCGC GTCAGGCCAGAAGAAATACAGGCAAACCCACTCCACGATGATTGCGCCGATCAGCGACCCGAACATCACGCCGAGAAATT GGAAGGGCGTACTGATGATGGTGCCGAGAAGGGTCTTCTGGCTCTCTTGTTGCTGCTCTGCTCGTTGAGTGACTTCAGCC ATCAGGCGGCATCCTCACCGGTGCCGAGGTGACGGAAATCGTCGACCAGGTCCTGGGGCAGACCATCCTGCAGGGCGGAG CATCACCTCGTCGGGGGGGGCACCGCCAGCGGCATTCGGATCTTCCAGAGATTGCCGCCCTCGAGTAGCGCGAACGCTT GTCCTTTGGGCAGACCAATGATGTGGGCCGGCTCGAGCATCGGCACGCTGGTCATCTGCACCTGGTCGTGCGAGCTGGAG GAGCTGATTGGTAAGGAGTTCGGCCGTGGCGGTCTCGCGCACCCGCAGCATGAACAGGTTGTTGAAGTTGCCGATGATCT GACCGGCCTTCGCGCGGGAGCCGATCTTGGCCTCGATGTCGCTCATGGTCTGGGTGTAGGCCGTCACCTGCACGCCGGCG ${\tt CCGCCCGCTTTGTTGACCATGGGGATGAACTCGTCGCCAATCAGCTCGTTGAACTCGTCGGCATGCAGGTTGATGCGGAC}$ CTTGCCGCTGGCGAGCCGGGCAGGCCGTCATCGACACCATGCTTGTAGATGTGACCCGCTACCGAGACCAGGTCGC TGAACATGGAGTTGCCCACCGCGGCGGCGACCTCGGTATCCGATAGTGCGTCGAGGCCGACGTAGACCACGGCGCGTTTG CGGATGACCTGCATCCAGTCGAAGATCGGCCGCGGATCGTTGAGGTCCGCGTAGTTGGGCGAAAGAAGCTCCGAGATCCG CCCGGTAGTGAGTTTCTCCAGTAGCGGCAGCAGCGAGCCACGATCTTGTCGAAGTAGGTCTTGTCGTAGCGCACGGCGC TCTTCAAGCCTTCCATGACCGGGTCGGCGATGCGTTTCTGTGTCAGGTACTGGTCGATGGCTACGACCCGCAGGGGCCGT CCTTTCATGTTGAACGGGATGTTCTTGTCGTTGAGCTTGCCCTCGATCTGGATGATGGTGTCCCAGGCCCTGGGATCGTG CTCGCTGATGTATTTCTGCGCATATTCGACGAACAACGCATCGATGTTCACGACGTGCCGGAGGATCTGCTGGTAGTCAG GCGGGGTTCCAGGCCACGTCCCAGGCAGTGGCTTTGGCGACCAGCTTCAGGGGGGAAGGGGGGGAACTCGAGCTGCTTCTC GGCGAAGCACAGCGCGACGATGCCGAACAGCGGAGTGAGGGAGAACGTCCACGGCGGCGACGATGCAGAGCGCGGCTG $\tt ATGATCAGGCAGCATCTGCACCAGCAGCTCGCAGAGGGTCGACTCGTCCTCCAAGGCCTTGGACGTCACCTCACCGCCGT$ AGCGTGAGATCAGTCCGAGCAACTCCTGGTACATGAGTTGGCGTGCCTGAGCGTCGCTCGGCTGCTTGATGACTAGGGTG ATCAGATGAGTAGTCATGAGGACTCCTACTGCTGGATGGCGGTGGATGTGATGAGGGCGGGGTAATGCTGCAGCCCTAGC $\tt CGGTCGACCAGGTCGTCCGCCGGCGCAATATCTGAAGTCCTTTCCCCCAGGCCCGGATTTCCGTCAGGCGCGCTTC$ GCGTGTCGTCGCCGACCAGGAACAGCAGTTGCAGGCCTTGGAGCGTTGATGGCGCGCCCCTTGGACCCGTCCTGGCGATAGG ATCCAGGCCCTGGTAGTAGGGGAGCGCCGAGGCGCCGAGGTCTTCGACAACGATCAGCCCGGCGGCCCAGGCTTGAG TCGCGAACGCCGTGCAAAATGCCAGCGTGGCAAGGAACTTCTTCATGGATTGGTCACCAGTAGGTTGACGCCGAGAACTT TGGATCCAGTCCACCGGTCTTCCCGGGGGGGATGCATACAGGGCGTCCCGCTGCTCGATCAGGATGTCGGAGGTGGCGTC CAGGTTCTTGTACGGATCCAGGGGACTCGCAGGGGCTGGAGAAACGATGTCCGTTCCAGCCGATGTTGACCTGGCCGAGGC CGGAATCGACGCTCTTGGCCCCGTAGAGGTTGATCGCCGCGAGTAGCGCTGTGCAGGCGGCGGTGCGGGTCGCGTAGTAG TAAGATTTCCCGGCGACGTTCAATGTCCAGGGCCAGGGAACGTATTCGCCGCGCAGCAGGACCTTGCTCTCGGTCAGCGC GACCGAGTAGAGCACCTCGGCCGGAACCCCTTTGGGCAGGGCGATTTGCTTGTACGCCGGCGGTGGATCCACGGCGGCCT GAGCGATGTTGACCAGGACCAGCAGGGTGGCCAACTGGAGGGCTCGAACTACAGACGTTGCCATCGGCCGTTCACCTCCT CGAACCTTCTTCGGGTCGATGCCGGCGAGGATTGCCCAGCGCCGCACTCGCTCTGCGTCGTTCTGGCTACCGACGAAGTA GAGGTCGAACTCCTTTTCTGCATGTTGCAGGTCGCGGACCCGCTGGATGCAGGCGGTGCAGTTGTCCTGGACGAACAGGG CCAGGCGCCCGCTGCTCTGCAACGCTGGGCTCATGTTCGGCGTGCCCGACGGGTTGGCTGTGCTGCTTTCGGTGAGGCGG CCGTTCGGCCTGGACCTGTAGATCGGCATACCGCCGCCGTTCCTCTGCCGATCGCGCCTCGATGCCCAGCGCGGTCAGCG

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FIGURE 2F

 ${\tt GATCAATACCAGGCGAGTAAGCGCCCCGGGGGCCTTGCATGAGCGTCTGGTAGCGGGTCCATTCCTGTTGGTTCAGTCCCC}$ TCGGCTTGCCGCCCTCCTGGCCGGCTGCGGGATAGCTCAGCAGCAGCATCAGGCCGGACAGGAGCGATACGGTTCTGA TCATGGGCGGGGTCCTATGGTTGGATGCGAACGCTGCGCGAGGTGCCGGCGACGTCGAAGTGCGCGGTACCATCGTCAAG GTCGGTCAGTCGCCAGGTCGTGCCGGCGACGGCATCTCCCCGGCGAATGAGGTAGATCTGGCTGAGCTGGGTGGATCCCG GAGGTGCAACCGACAGAAACCGTTCTCCCCCGCGATACTCCACGCCAAGGATCGAGAAGGGCGGGGGCTCCATCGGTTTG GGTTTCGGCTTGGGCGGGTATGGGGGCGTTTTGGCGCTGGCACGATCAGCGGCGCGCCCTTGGCCTGCTTTTCTTG GATCGCCTCCAGCGAGGCCTTTTCCGCGGCACTGTCCACGCCTGATCGGAGCTGAACGAGTTGGTACTGCTAGCTCA GCAGGCCGGCCATTGCCGTCAAACAGAGGCCAAGAATCATTGATGCAGGGGATGGGCGTTTCATGAGGGTCCTCGCGCGA AGCTGGGGACAACCTCTCAGACGGACAACGTTGATGCAGTAGGAAATACTCGGCGGAAGGGGGGAGGATTTTTTGAGGGG AGAAATTCTTGCGAATCCTCCGGCCTAATGCTCTGTGCGAAGCTGACGAAGCTCGGGGGCTCTTCGTCGCGCATCAGGGC TGAACGCTGGATAGCACAGCAGGCTGACCTGCACCGAAAAAACCAAGTGATTGGCATCGCCGCGTCGCTGGCGGATCGAC GATGGGGCGGACTCGTTGAGGTGGAGTAGTCAGTGAGGTCATTCGGCTTACCGGCAGTGCAAATAGGATATCCCGCTCCG TGACCGAGAGGATCAAGCGGCGCGCATGTCTCAGATGTCTGTGCGGGTGTGGTGGCAGAGAGTTTCCCGGCTGATATTC GGAGGTGGGGAACAATAGAACCAAAAACCAACGTAAGCAGAAATGAGTGCTGCACCCAACAACGCCGCCACAATGCCACT ATCGATTTGACGATACCGGTATACGTAAAAGCATGGAGAATCAGTATGTTACTCACCCCAGACGAAGGTTAGGTTGACCA TTGCGCTGCCTTCTGAAGTTATGGGGCATAGATTATGGCCGAAGCTATCAGAAAGGATGCAATGATGACAAAACTCTACT TTGATCTTCTGAACTCGCCTGCCGAGGCTCATTCGTCGATACAAAAGTCTTTATCTGTGCAGGCAATCTCCACAACTGTC CCAATACTGGAGTTTCCTTCGGAAACCGTATACGCCTATGCATCGTACATAAATGCATTAAGTATCGGTCAACGCATAGA TCCTGCATTCACCCAGAGCTTAACGAGTGCCATATCCAACCTGGCAGGTCGCCCGATTGCAGTAAGCGACATTTACCAAA AAATTCATGAAACCACACTGAGAACACCTGTTGAGATGGGCGTTCGTCCTAATAGCATCACCTTTGAGGAGTATCAGGCC ACCATAAATCAGCAAGCCATCAACATGGTTCAAGATATGCAGGATGGAGACAAAGGTGAGAAGGTGGAGGCCCTCCAGGC CAATATGCAGTTCCTGTATGGACAGGAGATAAATACTGATTTCATCGCTCGTAATGAACTCGCTGGTGGGCAGAGAGCGA AAACCGTCGCAATAGTTCAGGGGCATATCACCATCGGGTACGGCTTCGATACCTTCGTGCATGAAGCGTCCGAGCTAAAC TCTTTGAATCTTGTTGGTTCTACGCGACAGAAGGTATTACCTGCATTGCAGCTATCAACGTCCGACCCAGGCTTCTGGAG CGTCTATGCCTTGCTGGGACAAAGTCTCACGGATGACGATGGGCTATTACTCTTTAGTGCCAAAGCGCGAGCTGTTGTTC AACGCATAGCAAGCAACCAGTTTGCAGGTAAGTGGAATGGGCTACCCCCAGCTATCAAAACGGTTGCGCTTGATCTATAT TATCAATATGGGCAGACTGGTAATTTTCCAAAATTTCAACAAGCTATAAATAGCCATGATTGGCCGGCAGTCATCCATGA CAATATCCTTCAACTATGAGCAATGAGGATATGGATATGAACAACACAGTGAGCGAAACGCAACAGATCAATATTTACCA AGCTTGTGGAGGCTTGGGATATCCCTCTCGTACTCCATCCGGAGTTTGTGCCTAACGGAGATGTCTCGAAAATCGATAAG ${\tt GAGTACGGAACGATCCTTGCTGAGTCAGCTCAGGTTATCCTGCTTCAACTCCAAATGGCTCAAGACAAGGCTA$ GTGCGGGGAGGTTACAGCCTTGATCAGTTCTGTCTCCCAATCTCAATACCATTAAGAGTCGTCATGGTGCTAATTATC CAGTCTCAAACAGTTGCTCACTCAGGGAATCGGTGTGAAGCTTTCTCAGCCTGAATATTGGCCTGCTTACAACAACATAG CCACTGGTATTCGTTATACAACCGGAGTGGCGATAACGTTGGCCTATTGGGCCACGGTTTAGAGATGGTTGAACATTAGG ${\tt GAGAAAAGGATAGGTGCCCAGATCAATCTGCTCGTTCATTTTTTTGCTCATATTCGCGCCCACAATGACCCAAGCTGCGA}$ AAATACCAGCAAATGAGTACTCATTGGGGGATGGAAGGGCTACATCAATATCTGGCCGGAAAAGGATGAGGCTCAGGCA TTTCTTATCCATAATGATGGGCCTAATGGGGCTACATGCAGCCTTAAAGGCACTCTTAGAGATAATAAAGGAGTGGTGCA ${\tt TTCGCCGTATTCCTCTGCTTCATGTTTGCTAAGTATCACCCCAGACAGGGCTGCTGTCAGTAAGCGTCAAACGTGAGGAAA}$ TATATGCAAATAAGGAAAAAACTCGACAAATGTTGGGTATGATTGAGAAAAAAGAGCTTGATGCCGCTCGCGCCTTATC AAATAAGCTTTTGTCAGACTGCGCAACCGAGCTAGCCTATCCTGCCAAGATATACTTGACGAACACACTTGCCATGATCA $\tt GTGCTGAAAAGGGAGAGATGCTCGCTGTTTGGAGTATGCCCCATCGGGTGCAAAAGCAAATTCCTGTAAGAGATGACGGC$ ATGCAGCGACGAGAAATAATGACGCGTCGTAGTAGGCGCCTAGTTCACTAGGAGCGATCTTTTCCGACTCTCCCGCGGCA ACGGCCAATACACCTTTACTTAGGTTGAGCCGTATCAGCAAAAGAATCGATTCATATGTGTGAGGTACCGCCTCATGCAC ATTGGCTTTGGTACCGACATCTACTCGGAGACCCTCGTGCCTTGGTGAAACACCATGTGCCAACCATCTTCGTAGGTTTT CCAAACAGAGCTACGCATTGATAACGACTCATCGCCATTAGCATTTTGATGACGGCATCGGTACGTTGCTAACGCGACAC ${\tt CATCTGCAAGCACGCAGTTTGAAATCCTCGATTGTCCTTTTGATCCAAGTCTGGGATTTTAGTCCCACGATCACCTCC}$ GCTTTCGTCCAGCTTTTGCCGATAGCTCCAAATTCAACGAAGTCTTCGGTAAGCAGCTGTTTAAGCAGTCGATCATTCTT TCTCGATTCCGGCTCTAGCAACAGCTGTTCAAGCGCTAAAATCTCCAGGCGAATATCCATTTCCCTCACCTACCAAGTAT GATTTATATATGTTTCACAGGGGACAATAGATCACATAAGCTAGATCTGTACCCACTGATGCGGCAGCAACTGGCTGATG TCTTTCGACCGTAACGTCGGCAGGCGAGTTAGCACGTCCTTCAGGTAGGCATACGGATCATGCCCGTTCATGCGAGCGGA CTGGATCAGGCTCATGATAGCTGCTCGTTTGCCACTGCGCAGCGATCCGGCAAATAACCAGTTCGAGCGTCCGAGCG CAGCGTTTCAGGCTGTAGTCGAGGGCTTTAGCTGTGGCCGAGCCGTTGGGCACCAGGTCGCGCTGGGCCAACATCCAGTC GTTCAACCTCGTACAAACCGCCAATTGAGTGCAGCGCCTGTTCGGCCAGTTGGCTTTTGTTAGCGACATGCAGGTCGAAG AACTTGCGGCGAGCATGAGCCATGCAGCCGATTTCAGTGATGCCTTGTTCAAAACCGGCCTTGTATCCAGCGAAGTCGTC GCAGACCAGCTTGCCATTCCAGTCGCCTAGGAAGTTGCGTGCATGTTCTCCGGCACGGCTTGGGCTGAAGTCGTAAACCA ${\tt ATTTGCACCGGTGTTTCATCGGCGTGGATCACGTCCTGGTTCAGCACGGCTTCACGCAGTGCATCGACCAGTGGCTGAAG}$

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Applicants: Laurence Rahme et al.

FIGURE 2G

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 $\tt CCGCACGCCAGTTTGTCCGACCCACTGCGCCAGGGTCGAGCCGGCCAATTGGCAGCCCGGCGCGCCAAAGATTTTTTCCT$ GTCTGTACAGCGGCAAGTGATCGGCAAACTTGGCCACCATCACGTGGGCCAACAAACCTGCGGTCGGGATGCCTTTATCA ${\tt GGGTATTTCAGGTTCGTGGCGAATCACCGTGCGCGGGAACTGCGGGGAACGTTTCGGGGATTGCCGTGGC}$ TCGGCTTGTGGCGAAGCTGGAAGGAGTTGTTTCAGCTCGGCCTCGATAGCTTCAAGGTCGGTGTCGAGCAGGTCATCCAG ${\tt CAAGCTGCCTTGCGCCGAACTGATTTGCTCGCTGCGCTTGGCAAACTTGTGGCGTTTGAGCAGAGCGATTTCGAACTTGAACTTTGAACTTAACTTGAACTTGAACTTTGAACTTTGAACTTAACTTAAC$ ${\tt ACTGTTCGATGAGGGTTTCATTGTTGCGGATTTTCCTGCTCATCGCCTCGACCTGGGATTGCAACTGCAACGCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCAACTGCAACT$ GCGATGCGACGACAAGTAGACCAGCCAAATGGCCGGCGTTTACAGCATGCTGATCACACCGCCTGTGCCGACGCGCTGCC $\tt ACGGCAGGCCCAGGCACCAAGGCCTGGAGTTGTTCGCTGTCGAGTTCGACCTCGCAGCCATGGCGAATGCCGGGCCAGTGGCAGTGGCGAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGGCCAGGCC$ GCGATTGGCGAACAGATAAGCGCAGTGCGGCTTCGCCGCACCGAACACCGCAATTACCCGGGGCTAATGCCGTCTCGGTGC ${\tt TCGGCTGGCCGTTTAGGGGTGGCCTTCAGCGGGACAAAGGCTGGTAACGAGGCTGGTACGGGCTGGTCTCGATAAAGCGT}$ AGACTACGAGTCATGTGCCGATGCAGTAATTGACTTGCCAATGAAGACAGTCAAGATTGACGCTTTAGTAATAACGGAAA TACATGCTTACCCATGAACTGTATTCCGTTAGATAAGGAGCTGACTTTAAGTGAGTTCTTGTAGCCATAGAACTCCCCAA GACCATCCCCGTCGGGAATTTCAGTGATTCCATTTGCAATGACCGTATGGCCGCCTAAACCTAGAAGCTTGGGAGCATAG GGAACTGCTCCATCTGAAACATAAAGGGTGGGTGAGCGATGGTCTCTATCTTGCTTCCAAGAAAAGTACGAGTGTATAAC TCCTGCTAGTACCTCGCTAGCCGGATCATTCCTGGAGAAGAGTACGACATACGGCCGCCATCGACTCTCATGCTCACATG TTGATAGATCGCTGACTTTATGGAGAGGGAAGGGGAACGCAAGGGAAGTTGGAGGAGCCAAATACTTGATTACGAGACTTTG ${\tt CATGCTCATATGCACTGATCTCTAAGTGAGTTGACCATCCTTTATTACGTATTTCCTCTTGGATGTCGTTTTGGCAATAAA}$ $\tt CTGACAATTGACTCGATCCAGCAACGAGCCTCGGTACTAAGCGAAACGGGAAGGTTTCGGTCTCGCAAGTCAAGAAATCG$ AAATTTATTTAGAGTTTCTTCGACTTCTAATTTTTCTATTGCGTCGAATATATGGGTTGTTTGGATTGAGGTCTCTTTTG TTTGGGTTTCCAGTAAAACGACGGGGCCATTCTCGGTATATTCAAGGTCTAAACAATATAGCGCTTCCAGTACCCCCTG GTGTGTATCGTTGCGGCCACGGATCACCCAGAATGGAGCGCTTCTATTCATGCCAATGTGCTGCTCCAGTTTATCGACAT CAGCGAGTGAGCGGAAGCCGCGAGAAACTGCTACCGCATTTTGGCAAACCTTGAGTGGATATTCTGTTCCAAACACAAGA ${\tt AAGGAGTTCTTCTGCAAGCGTTTGGCATCGCGTTTCAACGCCGAGATGTTTCGTGAGGCGGACGCAGTGAGACTACGAAT}$ AAGAGATAAAGCCATGTTTTCCCCTTGTGCCGTTCGTGGCACTTACGGAGGTAAGGACTGGCTCGCTGTGGCACTTAGTG CCAATTTTGCGAGGTTCATATAGTGACAGTGCGTCCCTCTCGGGTTTCATGCGCCGCACCAGCGCGGCCAAGACTGTACC CCATTTATTAGATGACGCACAAATCTTGATTTTTTATCCTGCACTTCAGTGCCTATGTGGTGAGCGTAGAGTTATTTTC CGAAGGTGGCCTATGAGTTCATGCTGCGATGAGTTGTCGTGCCAACGCCATCTCCACAGAATCCCCATCCTGGTTCAACG AGTCGAGACCTGACTCGGGAACGTCTCCCGACGTGCTCTGAGCCACAGCGATCTTCTTGGCCATCAGCTGTAAGCAGGTG ${\tt CTGCTGCAGGGTGTACACGTTGTAGCCCGTTTGCAGGAACGCGATGGTCGGGAAGTCGAGCAAGTCCAGCCCGGTCTTCA}$ CCAGCTCCGGGTTGGTGATCAGCACATCGATGCCGCGATCGACCTGGTCGAGGATCCAATCCTCGCGTCGAGCGGTATCG ACCGAAGCACGTAGCACTGCCACCTTCAGCCCGGATTGCTCGAGCACTTTCTTCAGCCTGGACGTGGTGTCGCGCGTCCC GCTGTAGACGGTGTATGCCAGAACCTTGCGGCCCTTCGCTTTCTCCTCGAAGCAGGGCCCCCCAGCACCTGCTCCTTGG GTATCAACTGCTCGTCACCGAAGATCGCTGGCACGAAGGCCAGTGTGTCCCGGGTTCGCGGATGCTTGACGATCTCCGGT CGGAAACAGCAGTCCGGCCAAGCCAGCAGCACGTTGAGGACCACGCCCAGGAGCGTGGTATCTCGTCGCGCCAGAGCCTG GCGGAGCTCCGCTGTCAGCGTGGCCGCCAGGCGCTGATAGGCCGAAGCCTGCTCAGGCGCCATGGGCACGTCGATGAACT CCTCCTGGTAGTCGGGCAGTACGTTGCCACCAATATCCTTGAGCTTCAGGAACACGGTGAACGGCAATACGAAGCGGTGG ATGCCCTTTGGGCCGAAGCCGGGAGCCTTCACCGTGCGTACCGAGAGCTTCTTGCCCCGCGCTGTCTTGTGCGAATCACC GTCGCGCTCGGTGTAGATATCCTTGAGCACACCGTGGTCGCGCATGAACGACATGGCTGCGGGAGCCATGCTGCCGCGCG CGTTGGGCCGATAGCCGTCCTCGATCATGCGCTGGGTGAGGATGCGGAACAGGAGATAGAACAGATCGTCGGCGTAGCCG GAGCAGTTGGCCGCCGGCGGCGCGTTTCTTCCAGCAGCCGAGCCGCCAGTGGAAACCCATCCGCATCCGCACGCGGCCGA GCGATTGAGCGACTCCAGGAGCTCGTCGCCGAACTCGTCGATGAAGTCGGTCAGGTTGATGTTCAGGTGGGAGGCGGCGA GGGCGGCCGGTTGGGTCAGAGCGTTCATGTGCATCTCCTGCAGGTGAAGAACGGAGCAGGGCGTGCACGGTCCCCTTTGG

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FIGURE 2H

ATCGCCGAACTTCAGGGCTCTCTGGTTGGTGTTCCAGTCTTCCTGGTCCAGCGTTCCCCAATCTCCCGCCAGATGGCGTT TCAGCAAAGGCGCTGGGTTGAGTTGACCGGTTTCCACCAGGTGGCTCACGGCTGCGGTCATTACGACCCGGCCAGGGCTG ATCAGCAGCGGTGCGGGGGCCGGGCTCAGGTTGGGGCTCTTCAGCTTCTTCCGTGGTCGCGGCCGAGGAGCTGAT TCCTCACCTCGGTGATGTTGCCGTCGTCGTCGTCGTGAATTCGGTCTTGCGGACCTTGTCCTTGTAGGTGTCACCCTTC ACGACCAGGATCCGGCCCGACTTCGATCGCACGACGCCAGATATCGCGCCGGCGGCCAGGGCCAGGGCCAGGTGCCAGCG AGACAGCTCGCGGACTGGTGGGCGGGCTGCAGCCCCGCTTGCGCGAAGTGCAGGTTGAAGTCAGGCCAGAGACCTCGCA GCCGCTGGATTTCACCGGCGAACTGCTCCGGCTCCAGGGTTACTCGGTAGAAGTGCTCCAGCTCGCTGGTGGCCGGCAGA ${\tt ACCACGTAGGGTTCCCACGGCCAAGCCGCTGGAATTTCCTCGGCCTTTTCCTGGCCCGCTCCGATCGCCTGCAGGCGAGA}$ GGAACAATCAGAACCATGACGCCGCCGTACTGCAGCAACGGCAGCGCAGCGCTGGTAGAACGCTTTCTCCAGACGCCGGCG TCGCGGTCGTACTCGACAGCGAGGGCTTGGACCTGATCGCGGCCGAGGGTGTGTGCTGCCTCAGCCAGGGCAACACCCTC ACCGGCGCAGGGGTCACAGATCCTCATCCTTCCCGACGGGGCAAGAGTGAGGGCCTGCAGAGCGCGTTCGAGGGTGACCT TGAGAGGGATGGCTCAGGCTTGCGCCTGAGCATCGGTGGTAAGAATGCTTTCGCGGATTACCTCACCGAGGGTGGGCTCA AGCACGTCGACCCGCAGGGCGAGTCGCCAGGCGCAGACGTTGCCGATCGTCCCGGGTAGGGCCGTCAACATCTGGTGCTG AACAGCCAAAGATTGAGCAGGCTGCCGAACAACGTGCCGCGGAACTGACGGTGGTGCGTTTCTCCAGGAGATCCTGGTT TGGGAAGACAGGTAAGCGGCGGCCGTCCACGATGATGTGGAAATGGTCGATGCCATTTTCTTCCCGGCCCAGCGTCAGCC GCGTCGACGTACAGGTCTGGACACTCTTCGATCTGGTAGAGCGGGGTGGGACTGGGCATAGGAACCTCCTGGAAGGAGGA GCCACGCCGCCTCAAGGGGCGGTGAAGCCCCTCGGGGTGTAGTCCAACTGGTGCAGGGGAGCGTGGTGGCTACCGAACG CTCTTGGTGTGAGGGTCGAAGCTGAGTCCATCGGCTTGGTGCAGCGGCCCTTGGCCGATCAGGAAGACCTGGCAGAGGTA CTGATCGCGTAGCGCGACAGCCGCTTCCGCCTGCTCCAAGGTCAGCGACAGCTCCTCGATGAACAAGTCGATGAGCTCGT ${\tt TAGTAGAACGGGCCGGCGCTTTCCGGAATGGTCTTGTAGCCCCATTGCCCGGCCGAGCAGTCCAGCAAGTGCAGCTCGAT}$ CATGGTGATCGAGTGACCGGCCGGCTTGCCGAAATAGAATCCGGCAAGGTGAAAAGTTCGTTTTACGACAGTCCAAAGTT ${\tt GGCAGGGGGTGGTAGGGTGTTGCTTCAGCGTGTTGCGCGCTCAAGGCGCTGGAGGAGCCGGTAAGCTGTTTGCCTGGCCT}$ GCCAGTCGCAGTACAACCAGGGCTCGTTGTCGGCCGCATGCTCCGGCGAAGGGGTCTTCACCCGCTCACGCAGTGCGATG ATGGCCTGGTCGACGACGGTCGAACACTGCCGCGCGGAACTGGTCAGCCAGATTGTCCAGTCCGACCTCGCGCAG CGAGGCGCAAACCAGCAACAACTCCTCGCTGAAGCCTGGGGTGTTGTAGATCGATTTCATGCGGCCTCCTTGCGGGTCCA TGGTGTCCAGCTTGACGATTTCGCCTAGCGGCCAGACCGTCCCGAACAGTTCTGCATCCGCGTCTGTGTCCAGAGAGGCC GCCTGCTCTGCAGGAGCCGGAGTGTCCATACCGAAAGGCGCGTCCCTGGTTGCAGCGAGGCACAGAGGCTTCGACTTCTG GGGTGACGGCGACTTTGGTGGTATCGCCGGTACTACTGTGGGGAGCTGGATCTCGGGCACTTCGTCGAGCGGATCCACCT CATTGCCGGAAAGACGCTCTACCTCCTCGTCGCTGAGGCTGTCCATATCGTTCAGCGTCATGCTGTCCACTATGGCGCGC TTCGGTGTGTTGATCCAGGAAGGCATCCTTGATGATGAACTCCCCGATCGAAGTCCAGAGTTTTCCCACATTGAACTCGC CATAGCGACCGTTGATGGTTCGAATGGCCAACTGTCCGGGAACTGTGATCATGGTATGACCTGCGAAAAGGATGATCCCG TGTGGTACAGGTGGAATTGGATGTGCTTCGCGGTCGGCTGGAGAGAAAGCTCCTGCCAGGCGGTTTGAACGACACTGGCC GGCCTCTCCCGCGGGGATGAAGTCCCCGCGTGGGTGGGTAGGATGCACTCCATCACTTGCGTGATGCGACCGCGCTGCCG AGTGCTGTGGCGGTCTTGGGTGGGTTAGCGCTTGCGCGCCCGGAGCCTTAAACCCTGGCTCCTTGGGAGGCGCTGTCAACG TTGAGCGTGGGCGCGAATGGATCAAGTACCAGGAGCCGAATGTCTGCTTGTCCCGCGAGGTGAAGCAGATCGACAAGGTG ${\tt TTCGTCGAGGCCGAAGGCAAGCTGTTCTTGTCGAAGAGCGGCTGCGGTCATCTCCAGGATCTCCAGACACTCATCCGTCCC}$ AAGGGGTGTTGTGCAAGCGAAAGCCCACGGCACCGTGCTCGTTACACCAGAAGAGCGATACCAACACCGAGGGCAAGCGG ATTGGCATCTTGGTCGAGAACCTTTCGTAGAGGCTATTCCACGCGCTGATGGGTAGATGTGTTTTTCTGATCTCCCAGCA GGGGTTATAACCGCCGCCGAACGAAAGGTATCGAACGACACTCTCGGCTTCGGTCAGTGAGTATTGATCTCCGATAAGCT TTTTTCTGCCGTCCTGCTCACCGTAGATGCTGTAAAGTACGTTTCTCACTATTCCTTGGTGAGGGCATTTTTCAACTCTT TCATCGTCTAACTCTTGGACTACCACGGCGAAATCGTTATTGAAGTAGCACAGCTCGCACTGAAAATATTCGTCTGGGAG GTGCTGCTGGGTTTCATGCAGAGCGCGGTAGCACGGTAGATTGTTGCCTTCGTCAGTGATCTGCAGGTTTCGCTCGATGC AGGCTATGGACCTCCAGGTGAGTAAGGGGCGCCGAAGCGCCCAGGTGATGTCGAGTTGTTGCAGTTAACGCGATAGGTGT TCTTCTTTACGCCGAGCCTTCTGGTATCGCTCTACCAGGCCATAGTATTGAAGTACCGGTGATGTGCTTGAGTCGCAACC ATGCTCACAGTCGGCCTGCGCCAAAGCTTCGATTGCATCTTGAATTACATAGAGCTCGATACTGAGTCCGGCATCGCCAA ATTCATCAACCCGGCCTTTGCACTGGATGTACTCGAACCTGCTTTGTGCAGCATGCACTCCAATGTTGAGTAGAGCTGGG AGCCTTTCTGGATATGTGTTCATGGTGAGTTCCAATTCGTAATCAAATCGGAGAGGTCACCTCCCAGCAGGGGTGATGAC TAATGCCTGTTGGGCAAGTTCGCGTGAGGGGTAATATTCAACCGACTCGCGCGAGGCTGGTCCTTCTTCGTCAGAAGTGC

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CGATGTAGTAAGCACGGTTCTTATTCATAAGTACCTGCAACGGCAGTTCCAGGCTGAGATGGGCGAGCGCCAGCTTTCCG ${\tt TATTGCATGGTGATTCTCCTTTCGGTAGGAAACACCAGTCCCATGGGGACTGAGGTCCCCTAAATGGGAAATGTTTGGCG}$ GATGATCTCCAGATAATGGAGAACACCACGCCCTGGGGGGGAGATGGTGCCCCCCGGATGGGTATGCGATGAAGAGTGGCG GACGGTGGTGCCATCCACTTTGATCCAGGAGATGAAGAGCAGCCGGCCTTTGAGGCTTGCGTCGGGCTTGCCTTGTTTCT GCTTCCTTGCAACGGCGGACAAGCTTTTCAGCCTGGGCGCCGACCACTTTGCAGTCGATGTAGGAGTATTCCACGCTGTC GGTAGCCGATACCGGTGGTGTGCAGGTCGAAATACTTGGCTTCTTGGGCTTGGGTGTTGTTGCTCATGATGATTCTCCAG TTTCGTAAGCGAAAGCGGAGAAACACCTTGCCCGTCAGGGAAAAGTATTCCCCGCATGGGTCGGTATTGGGAGGTAAATC A GAGGGAGAGGGCTTCCATCAACCTGTGGGTTGATTGATCGCGCTACCGGAAGCTGGTGCGATCTTGGGTTCGATCTACACGGAAGTCCGTGTCGTAGTCTTTCAGATCATGACTACTGGGGGAGGGTTGCCGACAACGTCAGCAGCTCACGTGGTAAAG GATGGGCAGGGGAAAAATGAATGTCAATACCCATGAAATGAAAAAGCGCCCAGGGTTGGGCGCTTTCATGGTCAATGAT GACGGGGAAGAATCCGATGTTTTTGGCACCAGGTCTTGACCTGAGGCCAACTGAACCAGAGGGCTATGCCGGAGCAGATA ACCACCAGGCTGGTCATGATGATCATGCCGAACTCGGTCTGGGACATTTCACTCCTCCTCGGTGAGAGCGATACCTATGA GCCAGATTACCATACCCATGACGAAAGCATATGCCGTCAGCAAGCGGTGCTCGCTGAGGAAGATGCCCACCAGGCTCGCC $. GCAACGGCAGTGGTACCGATTTTTCGGAGATCGTCTGCGAATGCAGAACGTTTCGATTTCATGGTTTTCCTCGAAAAAT{{\tt G}}. \\$ $\tt CCGGAAAACCACCCTGCGGGATGGTTCCCGGCAGGGTTGGGGGTGGTAGCAGTGGCTATTAGCGGCCGAGAGCAGCTACT$ TGTTCATCCGTCATGGTGGACAAGTAGTCCTGCCAGCGTTGTTGGTATTGCTCCTGAGTACGCCGATGGAGTTCCCAAGA ${\tt GACTGCGCTACCAGGAGGGGGCCTCCCCCA}$ ${\tt GCGGTCGCCTTGGCCGGGTTTGCGTCGCGCGCTTTGGGCTTTGCACCTCGCGCGTATTGGCTAGATACCAGTCATT}$ CGGAACTCACGCACAACACTGCCGAGGGCAAAGCCGATTTCGAAGCTGGTGGATTGCTTGGACATGGTGTTTCTCCTGCA GGTTGAGGGTGCGGAGAAAACACTGGCCCTGGCGGGGAAGTGGATTCCCCGCTGGGTTGCGGAAGGGAGCTTCTATCGAC CGAGGCCGACCGACCGCGCTACCAGAAGCTATGCGGTCTTGGGTTGGATCAACACGGTGGGCTGTGCTGCAGCATTTCGG ATCCGAGCTGCATGGGGGGCATGTCGCTGACAACGTCAGCAGATCACGCGTTCATCATCGAAGCGGGGGGGCGAAAGTGTCA GTTTCCCCAGCCGTGTCTGGAAGGGGAGTCAAGTGAGCCACCTGTGGTTGAATCGTCGATCCCTGGGCATTGATCGTCTC GATCCCATCACCCGGCCATTATCGTGGCTTGGCCAGCAAACAGTAGGCACGCATCCGCGTACAAAGGGAGCCCTGCGTAT GAGAGGGGAAAAGGAGGGGCCGTAACACCAGTACGACCCTTAAATCGAGGAAACACCGAACCTCTTGAGAACCCTATGTG CCTTTAAACTCGCTCGACACGAGTTGACGGCTGCATGACAAGCAAAAGAACAGGGAGACACAGGGAGAATTCTCAACCAG ATCCGCACGCCCCACCCGGTGTTGTAGCGTGCTTACGGTTTGGCGATGAGGCGAACCTGCATCACCAGGGCGCTACTGAT ${\tt GACCGGAAGAGCAGCAAGCTCCTGGCCAGGGTGTCGACCTCGGCCAGTTCGGCGCTCGAGGTCGCGTGGTCGCTTTGTAC}\\$ ACTCAGCCAGGTCCCGGTGATGAGCGCGAGCACCAGGACGATCCACATCAGCGGCATACGGTAGTCCTTGAGTCGTGGCG GATCTCAGTGATTAGCCCGAACGAGTAGTTGGTGCCAAATGTCTGGTTGAAGCCCACTGCGCAGAATCGGCCGCCGCAGG TGATCGCGTAGCGGACGTAGTCGTAGTTCACCATGGCGCTATCCTGACCATGCAACGTACACCAGTCCTTGATCACGCCG ${\tt GCCGTGGTGTTCAGGCGCGTGGAGGCGGGGGTTCGTCCCCATTTCCCGTTTTGGCAGGACAGCCAGAGTCCGGTGCTGGT}$ GTGCTGTCGCTCATGTACCAGCCGCCCCCATTTCTCGTTGTACCAGCCCGTGTCACCACGGGTCCTGAACCAGCCTCC ATCCGGTTGAGTTCAGGATGACCCGGGACGGCATTGCGGTAGAGGTACTCGTTGGCGATGGCGCCGTCCTGGAAGAACAG TGGTGTTGGTTTTCGAGATGTAGCCCCCGGTGGCTCCCATGAGCTGCGCGATCCGGCGGATCGAGAGTTCGGAAGCTACC TGTCCACCCGTGGTCACGATCAGCGTTTCGAGCTGGTTGGCCGCCGGCTTGCGGGCCAGGACCTGGTATTGCTGGCCGTA GATGTTGGTGTCGCGGAAGCCTGCGGGCAGGTAACGGGTGTTGCGCAGCATCGGGACGGTGATCACCGCCGGGGCCGTGG GCCGCGTGCTGCTCCAAGCCGTCCAGGTAGCTCATCAGGACCGATATGCCACCGGCGGTCGCGATGGCGATCACGAC GAGGGCGATCATCAGTTCGATCGAGATGAATCCACTGCTGCGCGTACTCCTCATGGTGTTATCTCCATAGGCTTTGCCGG GACTGGCGAGCTTGGTCGTCCTGCAGCAGATGAGCCTCCTTTCGGCGGATCTTGTCGCGCATGGACGGCCCGTCGTCGCC AGTGAACAGCAGTGGCTCGGCGGTCAGGCGCGCGAGGAACCATCGCTCTCCAGCGCTTGGCAGATCACAGCTTGGATGC $\tt CTTCGGCAACCACGTCGTAGGCGTTTCTCGCCAGTGGCTGGGCGAGCGTCACCAAGCGCTCGATCGCCTGATGACAGCTT$ TTCGCGTGAATGGTGGCGATCACCAGGCTGCCGGTCAGAGAGGCCTTGCAGGCCTGGTAGGCGGTGTCCTCGCGGAT CTCGCCAATCAGCACCAGGTCGGCGCCGCAGCGTGCGCAGCAGCAGCACCTGTATCCGCCTGAGCGCCGTGAGG GACCAGGCCCTGCAACTGCGGATCCATCAGTGCGGAAACCACTTCGCTCGGATAGCCGATCTCTTGGAACTCCCGCAATT GGGCGCTCGACCGGCGCACGAAGACGCTGCCACTGAAAGCGTCTTCGAGGAGGGTGACGCGAAGCAGAACGCCGTCG

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GGTCGACGAACTGAGCCTGGATGATCGGGTTCACACTCACGAACTATAGGTCCAGGTAATGCTGTTGCTGTCGCTGCTGC AGGCCTGGGTCGCGGCTGCGTCACTTCTCCGGTGATCGAGGATCCGCTGTTGATTTTGGTCTGCTCGAAGGTGTTC TTCGCGATCTTGGTGGCCAGCGTGATACAGGCGTCCTGGGGCAACTTGCTGGTGGTGATCGAGAAGCCCATGCCGGTGGA CGAGACAGTGACCGATCCGCCGTAGACGTTGTAGACGACGCCGGAGGAGACACTCATGTTCTTCGGCACGCCGTTGATTG GATGGCGATGATCAGCACGATGATCATCTCGATGGAAACGAAACCGCCCTGCGTCGGACGGGAAGTGCGTTGCGTAG TGCTCATGGAGCGCTCCTTGGTGAGGTTTCAGTGGTTCATGGATTGGATGAGCTGCTGTGCCTGGTAGGCGCCGAGCAGG GCAGCTTCCAAGCGCTGCTTCAGCCAGGCCGGGGAGATCTTGATCATGCTGGCCAGGCTGTCGTAGGGGCCTATGCCGGC GTTGAGCATGACCGCCATGTTCAGCAGGAAGGTGGTGCCCTGGAGCATGCGGTAGATGGACCAGGGCGGCAGCGTCCGGT $\tt CCAGCCAGACCCGGCCTTTCCAGCGGTAGGTCGGCAACGTGACGATGACCACCGTGAGGGTGATGACGGCGACCAGA$ ACGTAGATACCAGGTCCTGTGACGAAGCTGGCAATGGCGTTGAGCGTGGCGAGCGGGCCGGTCCAGGTGACTGGGTCGGA GAGCCTGGCCAGGCTGGGGACCATGCGATAGGCCACGATGCACAGCAGGAACACCATCATGGCGGACAGCGCCGAGGGGT AGAGCAGCGCCTGCCAGATGGTGGCGCGGATCCTGGCCTGGGCCTCGACCAGGGAGACGGCATCGCCCATGGCCTGAACC CTTGCCGTTGGACAGCCCCATCAGCGCTTCGCGACTGGCGATGGCCACCGGATGAAACGGATGCTGCCCCTCATGAGCGA AGATCTTGTGCACCTCTGCCACAGCATCCTTCAACGGGACCCCGTTTTCGAGCAGGGTGGACATGCTTTCGTAGAACTGC TGCGAGTAGAAGCTGTCGTCGAGCAGATGCTCATCGAAGTCGAGTGGCCCAATGAAATCCTCGACCATCTGCGGGTCGAA CATGCCCTCGTTGATGCGGGGGATGGCGTGGGGGGTGCTTGGTGATGCCCTGCATGGTCTTGACCCAGTAGTTGCGTGCCT ACCCCGGAGCCACGGCAGGCCTGGCAGCCAGGCCCCTTGACGTGAACCTGGGAAACATCGGTCAAGCGTCGGACCCGTTC ${\tt GACCAAGTCGGGCGCAGTTGGTCTTGGGAAGCGCACTTTGCAGTGGGGGCAGGCTTGGGCAGCAGGCTCT}$ GGTTGATCAGGCCGGTCAGCAGGGCCGGATCGAACAGCAAGCCGGGGTCGACGCCCAGGTCCTTCAGGCGCTGGACAATG GTTCTGCGTCTGGGTCGGTGGCGTAGACCAGTGGGGTCTGGTTGATGCCTTCGCCGCGAATGCGGTATTCCGGCGGA GCAGGTAGCCGAGCTGCCCAGGCTGTCGAGGCCGGTGTCGTAGAGCAGTCGCAGGATCATCAGGAACCCCCCGGCA TTGCGGCTTGAACAGTGGCTCGGCCACGTCGCACATGGATTGGTAGATGGTTGCACAGAGTTCGTGCAGCTCCTGGCTGC GGAACTGCTCGACGGTCTTCAGCAGGCCGTCGACGCGGAAACGGATCTTGCTGCCGGTGCCGGCGGGACTCACGACGAAA ATCGCTATCGACCAGGCCGTCCATGGCGACGGCGCGGTAAAGCTGGTGAATGGTCTGCAGGTCGGTGAGGTTGAGCTGGT GTGCCGTCGGCAGCCAGAGCCATGATTTCCTGCAGGTGCTTCGATACCTCCCATTCACCACCGTCGGCGGTGAGCAGTTG TCCGCGCCGCTGGCGGCGTCAACCTCGTACCCGCCCGGGAACAAGAACGTGGCAGTCATCTTGCCGCCGGCGCCGTAGAT GGTCCGCACCACTGGCGGAACCGGCTGCGTGATCGTCGGCGGCGCCGCCCGGCACCGGCATGGCGAACGTCTGCCCCTGGG ATGGCCTGGGCCTGGATCTCCGCAAGTTCGCCAACGGTGCCAGCGCAGGCCTGGCCAGACGCGAGGAAGAAGAACACGC ${\tt TCGAGGTTGGTGATGCGGACACCGGCAGCCGGCAGCCCCTGGAAGGTCAGGTCTGCCGGGAGCCGGGTCTGGGCGCTGAAGGTCAGGTCTGCCGGGAGCCGGGTCTGGGCGCTGAAGGTCAGGTCTGCCGGGAGCCGGGTCTGGGCGCTGAAGGTCAGGTCAGGTCTGCCGGGAGCCGGGTCTGGGCGCTGAAGGTCAGGT$ ${\tt GCGGTCGGCGAACAGGTGCTGGCCGCTGTCAGGTCGGCTGCTGTTGCCGGTACGGTGGTAGGTGGCGACCA}$ GCGCGTAGCATGTCCTCGAGGTCAGGTATGAGCGTCCAAGGCTTCTGCAATGACGCCAGGTCCAGCGGCTGCTTGGCCTG GGCGTTCTTCTCGGCCAGCTCGGCGAGGCGCCTCTGCTCCTCGAGGAGCGCGGCTTGCCTGGCGAGCTCTTCCTGGTGGG CATTCCATAGGTAGTAGCGGTTAGCGACCCACCTACCACGCAACCGAGCAGGGCCACTGCCGTCCACTCCCTGGCGGAC ${\tt AAGCCGAAGGTGAGTTGCCGGAGGCGGTAGTCGCGCCGCAGGCGCTTCGGCGCGAGCAGTTCCTCGATGTCGAAGTCCTT}$ CCCGGGCCTCGTCGAGGGTGGTGACCAGATCCTGCCCGGGGACAATCGCGCCATCGAGCGTGGCGACCAGCGCGTAGCGG ${\tt TCCTCGTCGACTTTCCAGCAGGCCAGGAAGTCGCCGTCGAACTGGCCTGAAAGCGCCGAGGCCAGGGAGTACATCCCCTT}$ GACTGCGCCTTGCGACTTCGAAACGAAGCCGGCCTGGATCACCGTCGGTGAATGGCGGATGGCAACGATGTCCAGATGCT GACGGGGGTGATCAGCACCACGATGACCTCGCGCTTGGTATTGCGGGTCAGCCCGCCGCCAAGACCGAAGAACCCAGCGT ACCTTCTGGTCGAACAGTTGTATGTCGTAGCTCGGGAACTGGGCTTTGGAGTCCCCGCTGGTCTGCATTTCGAACGTCGG $\tt CCGGGAGGTCATGTTGATGTTCAGCAGCATCTCGCCGCTTTCCATCACGAACGGCAGCAGGCTCATGTTGTAGC$

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FIGURE 2K

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 ${\tt AGGTTCCAGTCGATCCCCAGTTGATCCTTGTCGGTCAGGGCGACCGAGAGCACCTTGACGTTCAGCAGCACCTGCTTGGT}$ TGGCACGCGACAGCGACATGCGTCCCATGCTCGGCGTCAGCATCGAGTTGATGCTGTTCTCGATGTCGCTGAGGATCGAT GTCTTCAGCTCCGAGCTGGTCGTCTGCTGCCGGAGCTCGCCGCTGATGCCGGAGCTGCCATTCTGTCCGGTGGATCC ${\tt CGTACATGCGGAAGGTCCGAGTGTCCAGGTAGTAGAACTCGACCCTTTTCTCGGTTGGGTTGTAGCGCCAGGACACGCCG}$ CCCGAAGCTCGACCCCATGCTGCCGCCGGCACCGAGCGACATGCCGTTGGCGACGGAGGCAGGAAACAGCATGGTGGCCA TGTCCTGGCCGCCTTGGATGGGCGGCGGGGGGCGTTGCTCGCGCGTTGCTGAGGTTGCACGGCGAAGGCGGCCGGGTTCAGC AGAACACCACCGTATCGCGCCGATCCGGGTCGGGTGTTGCGCACCTGCGGTCGGATCGTAGACGCGGAATCTGCCGTAGCT GGCCGTTCGGCAGCGTCATACAGGGGGGAACAGCTCGGATACCGCGTCCTCGAAGGAGCCGTGGAAGGTCAGTGGAGCCTC GATCGGATAGTTGAGATCCTGCGGCTCCCAGCGGACGGTCCAGCGTGCGCGCTTTGCCCAAGCTTCCAAGGTGTCGCGCA -GCGGAAGCCACGGTGGGTGGAGTGGGCGGGGGGGTGGACTTCACGGCGGAGGCCGCAGGCTTGGTCGGTGCCGAAGCCGCGG _AGGAGAAGAGGGGTGGCCATCCTTGGCCGGTGCGGCTGGGGGGGAGCACAGTGGTGGATTCAGGCTTCTTGGCCGGAGCGT GGCTGGTTGTGATCGGCGCGGTGTCGGCACCGAGGCGACCACGATGGGCGACTCCAGCGTGCTGACTTTCTCCGTGGAG $\tt GGGAAGTTGATAGCCCGGGGCGCAGCACGAGCAGGACCTGGCGGGGCGGCGACCTTGACCTTAACCTGCCAGGCTGGGCCGG$ AGAGGACCTGGAGGGTGTTGCGCAGGGTCATCGGGCCGAGCTTGTACTGAGCTGCCGGCAGCGGCCGGGTGTAGAGGATG GGGTGTAGCGCCCATAGCGCACTACGGGCTCTTTCTCCGGCTGCACACCGTTTGGATACAGGTCCGGAGAAAGCAGGTCT GAGAGTGGTCAACTGCCTGGTCATTGAGGCCCCCTTTGATGATGGGGCCACACAGTGGCAGGCCATCCGCCACGCATCAGC ${\tt TAGGAGCGATGAAGGTTTTCATGTTACGCCTAAAGCGAGCCAGGTGGGAATCGTTGTTAGAAATGGATAAAATAGAAGT}$ TCTAATCGTTTTAGAATGCTTTGTTGAACTCAGGTCAGACAGTACGGGGTGCTAATTGAGCTTTAAATACTATTGGGCTA AATTTTTCTGGGGAGCTTTCTTCTTTTTTTTAGTCGCTTGGAAAGGCTCCGTATTTCCAAGCCTGGCATCAGTTAACCCC ${\tt TTGGTAGTGGCTGGATTCAGTACTATCCTGTTTCCTTTCTCGGTAAGGCTTGTTGAAGACTTCGCTTTAAAATATACGGA}$ AAAAGAGTTCTGGGTCACAGGTTTTTTCTCCGAAACCCCTGCAAAAACAGGATTGTATGCAGTCTTTTATTTGGCTTGTT ATTTGTTTTCAATTCCCTTGGGGATGATTTTTTTATTCTATAAATACGGAAAGGCCTCGTAGGATTTAACGAGGCCTTGC TTGGTTTTAAATGGACATTACAAGGTTGTTTGCTTTTTCTAGAAGGCCTTCGTCAATCATCGCCCCGGTAACTGCCATTA CCAGTGCGAACCCCAGGATGCCTATAGGAGTGGCCGTTGCCGTGGCAAATGCAATACCCACAAGCCAACTGGCGGCCGCA CCAGCAGCTAGTGTTTCAACTTTTACAAAGAATGGTTTCCAGTCCCCGGTTTCCGTAGATATCTTGAACTCTTGGTACAG ${\tt GCTGGCGGCGTCAATAGCTTTGCCTACAACTCCAAAGCCTTTGCTAAATTTCTCAAGGCTCTTCGCCATCATCTGCTTGT}$ AACGAATTGATTGCTTCCGCCGAACTCCTGATATTTTTCCCCCTGGCGCCTTCGGCCCAGTTGGTGCGCCCATCTCTGATGT ${\tt TCGTGCGCCAAATTTCTCAGTTACTTCCTTATAAAAGTCGGCAGTAAATTTAACAGCATCTTGCAACGCTTGTTCCTCGG}$ CCGCCTTGCGTTCTGCTTCTGCCTCGTGTCGTTTCGGCGTTCAGCTTATCTAAGCGGGTCTGTAGACTGGCTATC TCATCCACAAGTAGCTCACCATTGTAGATGGCTTTCTGCTTTTCTAGAGGGGGTTGGGGCATTCTTGATAAGAGTATTGTT TGTGGTCTGCAGCTGCTTTTTATCAGCAATTGCTTGCGTAACCAGTCTTGTGGCACGTTCAAGCCATTGCTCTGGCGTTG GACTGACCAATGGAGGCAAAGCACTTCCCGCTTGATCAAGCTCGGATTGTACTTTCATCTCGAGATTCGCCTTTCTGGTT TTGTAGTCCCGCTCCAGTTGAGAGAGGTCCTCTTTTTCCTTTAGCGCTTTTTTGCTTGTTGAGCTCCTGTCTTAGCACTTT ACTTCTTTCTTCCCCAAGAGTTCTTCTCCCAGATCTTGACCCAGGCCTCATAGATGGAGAGGCTTGACTGCTTTTCG TAGTCAATGAATGGGCCTTTGGTAAAGGTCTTTTTGTATCCTTCAAGATCAGATTCCATCTTGTGCAGGACTGCCGACAT GACATCGACTCGCTCTTGTGGCCTCCCTTTTTCCTTGAGTGATCTGCTTTAGCAAGCCATCGACTTGATCAGATA CTTTCTTGTTGATCTCCTTCTTTTCTTTTGTTCCTTGTTCAACAATGGATCGGACTGGATAATAAATGTTTTTCTGTAGA TATATGTCTCTTTGAATCAAGTCGCCAAACATATTCCCGGCAACGGCCGCGCTATCGATAGGGGGAACCTCGTATGCGTA TTGATCGTCTGGACCTTGTGCGACAATAACCATGGAACCAGGTACTTCGTTGTCATTGGACATTTAGACTTCTCCATTGG TGAGTGTGGTACAGAAACAGTGCCGATTCAGCTCTAGAAATTGAACCCCATGGCTTCAATGTGTGGGCAATGCACTAAGA AGGCACGTCAATGCGCTGATATAGTGGTAATAAGCACGGTTGCTTAAACTCGATATTCAGGAATGGGATTGGCTGAGC ${\tt CCACGGGATATTCCCTAAGAGTCATGTATCTCTAATAACGAGTTCATGCGCTCAAGATTCACGCTGGGTATGTGATGCTC}$ TCTGCAAAATTCAGCTACTTGATCCGCAACACCATTCAAGGGTGAAGATAGGGATAGCAAGCGAAGAGACAGTTTTGTGC GTTCCATGTTAAACGGGAGATACACGTCGAAGACCTAAGCCATTAAAACGTGCTGACCATCCAGTTGGGGCCCATTAGGA ${\tt TCTAGCACACCCATGGTGCACTGGGGCTATTTCTCGGATGTACACCGTTTTGGTACAGGTCCGGAGAGAGCAGGTCT}$ ${\tt GAGAGTGGTCAACTGCCTGGTCATTGAGGCCCCCTTTGATGATAGGCACAGTGGCAGGCCATTCGCCATGCTTCAGCA}$ ${\tt GGAAATACTCGGCGGAGGATCAGGGCTTTTTTATCCAGTTAGGCTTGCGGCTAAAAGCGCGCGGTTTCCGTCGACCTGCT}$ ${\tt AGTGGGATTTTCACCACGACCATGCGGAGCTGGCCGTTTCGGTACGCGGGGTCTTCGGCTTGTTCCTGCTGACCGGGAGT}$ CCAGGGCAGGCCGAGGAAAAACACGTAGTTCGCCGCAGTGAGGTTGTTGCCCGTCCCTGCGGCCGCCGTAGTGCAGATGA ACGCAGCCGTGTCCGGCAGAGTTCCTTCAGCGCAGCCACGGTCGGCTTGAACTCGCAGAACAGGATCACCTT

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GTCCTCTGCGTCGAGCTCGACAGGGTCCATCGCCACGCGAACTTTCACCGTTTCCAGGTAACGCCGCAGCGCGCCGA $\tt GTCGCGCGAAGACCGGTCGTCGTCGAGGCGCAGCACGTCGTATTGCTGGCGTTCCTCGGTGGAGAGGGCCACCTTCAGC$ ACTCTGGCGGAACTCCGGGTTGCCGGCGAAACGGTCGCAGAACTCTTTCAGCGGCAGTTGGCCGATGGGGTGGCCTGAGA GGCGCAGCAGGGTGTGCAGCTCTGTCTCGCGGTTGAGCACCGGCGTGCCGGTAAGCAGGTAGCGGTTCGGCACTTGGGCG GCAATGTCGAAACCGTGCGCGTGCATTGCGCCGTCGGTTCCTTCATCCGCTGCGCCTCGTCGATGACCATCACGGCGAA GCGCGAAGCGTTGGCGACGAAGGGGCTCAACTGCTCGTAGTTGACGAGGATCCACTGCGCCTCTGGGGTGTCCTGCTGGA TGGCCACGGTGGCCGAGGGATAGACCTCCTGGATCTCCCGCTGCCAATTGATCAGCAGGGTAGCCAGGGTGATGACCAGG ATTGGTCTGCCCGCCGCGGATCGAAGCGGCGATGACCGCCTGGCGGGTCTTGCCCAATCCCATGTCGTCGGCCAATAA GGCGCTGGTTCTCTGCAGCAGATGAGCGATGCCGTCAGGCTGGTGGGCCAGTAGAGAGTAGCCCTGAAGCGCCGCCTCGA TATCAGCCGAGCTGTACTCGGTGCGCTCGATCTCCGGCACCGCGGCGAGGTAGATGTCAGAGGCTGACTCGTCCTCCAGG GATGGCGCTGCCGGTTCCTGCTGGACCGCCGATGCTCATGCTGGGCAGCTCGGTCGACGGCGCGAAGCTGCCGTCGCT GAGCAGCTCCTGGACAGTATCCAGAATCTCGAATTGTTCCTCGGCGAGGCCAAGCTCCAGAATCAGGTTGCTTCGGAGCA GCTCGGGAGTGGTGTCGATGCGCCAGGAACTCGATGGGCGCAGGAATACCCCGCGCATCCGCCGAGCCACCACAACA CCAGGATGGAACTCGCCTGACAGTAGGACGCCGCCCTCGGCCAGGGGGCGCGATGCGCAGCAGCAGCATCCCCCAGGTGAAGGC CTGTCGGTCAAGCGAGGCCTGCGCGGATTCGACCAAGGAGCTGAACTCCCGCCAGGACTGGGAGTGAAGGCCTCCAGCTA GCTCGGCGAGACGGTTGTACAGAGTGTCCAGTTCAGGCAGCAGCTTGCCTTTGGGGACCCGCCAGTAGCGGTGCAACGGA GAAGTCGTAGCCGTCGAAGATAGCCCGCTGCAGAAGCGTCGAAGGTGTCGCGGAGGTACGATTAACCAGGCGTGGACGGT GCGTCATGTGGAEGGTCATGTCGGGCCAGTTCAGGTTCGTCGCTATGGCTCCAGAGCGAATTCGTTCCATGAACCAGCGG $\verb|ACTCCAGGGCCTACCTATAGGCTCGCCATGCTCACGCCTGAGCTCCAATTCGGCAGAGGGCCAGCGGACGACCAGCCTCAC| \\$ $\tt GTACTGAGAGCAGTCGGCAGTCTCCTCGGTAGGCGGCCTGGTCGTAGCTATCGATGCAATGTGCCAGAGCGATATGTTCG$ $\tt TGCCGGATCCTGCCAATCCGACGGGCAGCCGTTGAAGAGACGGTTGTAGTCGGGCTTGTGAACTTGCCAAGGGA$ A GAGCATGCCATCCCGAATGTCGGCCTTCCCGTTTGCGATGGAAGAGAGCTCCTCCCGCACGGCCGGGACTGACGTGACTAAGAAATCGAATCGAGGCCCGCGGCGCCTGAAATAGCCAGGCGAAAAAGTTGATGACCGAAATTCCTTCGTCCGCGACCT AGAGCTGGGGCGAGAGGCACCGAACCGAGCGGATGGCGAACAGCAGGTCTTGGTCCAGGACCTGTCTGAAGGTTCGCAAG GCAGGCTTGCACTCCCACGCACCAATTAGTTGACCGTCGAATACCTGGAGTAGCGGCCCTGCACGCATGATGGTGTAACG CACACCGTTGTCAGCAGCGACTGTGATGCACCAGCACCTGGTCGTAGATGTGCTGCGCAGGTAGTGACGGATGAACTTGG ACTGAAGGTCTTATTGGGATGGATCAGTAAATTCTCTTGTAGTCAGCCTCAAAGTCTCCTAGTGCAGCAAACTCGTCAAG GATAGCTTTACTTAAAAGAATAAGATGTATTGTCCTCGCTGGGTTGTCCCAGTTGGCACCACCATGCTTGCCTCCGTGAA ATAGATTGTTTCGCACGGTCTTAAGTAAGCGAGCGACTCTAGCTAAGTCGCTTTTGTCCTCATCTAATTTAACCGGACGC CAACCCAGCTCTCTACCGGGCAGGACTATTTGTTGCTCTGGACTCTGCTCGATTAGTGCTGTGGCTGATTGGGAAAGAGA GTATTTGTCAGAATGGTTTTGTACAAAATTTTCCCATCCCGGCTCTGCCCTAGCTCCAGGTTTGTAATTTTTTAAGTAGC TTCTCTTTTCGCATAAACCCTCCTTGATAGCTAGCAGCGAATTGGGCCTGTACCATTTTGCCTGCACTGCGTGACTAACT CGATAGCCGCTGCAACCCCAGAAGTCGAAGCCGCCTTTGCCGGCTTTCTTGCGGTGAACCAGGGGCAGACCGCACTTGCC GCAAAGGAAGTCGCTGGTCGGCGCCGAGGAGATACTGGCGGTGGAGCTTGCGCGTGGTTCGTCCTGTGCGCTGGGGAGCG CGCGGAGTGTCTGCAGCTCTGTCTGTAGTAGCTGGTAGAACTGCTGGACCACGTTCATGTAGGTGTCCTCGCTGTTGGCG GGCCTCTCCCAGCTCGCCGGGGATCAGGCTTCGCCCCTTCATCTGCACCTGGCCCTTGTCGATGATGTTCTTCACGATCG GTGGTTTTCTTCTCCAGGACCTCGCCGCTGTAGACCTTGAGTATCTGGCGTGGCTCCAGCGCCCGGGATCGGGATCGGGTT ACTTCAGCCCCAAGGCTTTGGCGACAGCACGGATATCCGGCATCGAGTCCTTCGAGATATTGGGGTTGTCCGTCGGTGG ${\tt TAGGTGATGAGCCCCTGTTCATACAGCCGCTGGGCGACCTTCATCGTCTTGTCGGGTGACCACTTCAGCGCATTCCCGGC}$ GGCCATCTGGAGCGAGGAGGAGATGAACGGTGCCGGAGGCGCATCGGTTTCTTCGCTATCAATGCAGGTCTCGACGATGA GGATCCCATTCCGCCGTCCAGGTACGGCCGTCGCTGGGCGAAACGAAGGTCAGTTCCACCCCGAAGTGCTTGATTGCTGT GAAGGCGCGGATCTCCCGCTCTCGCAGGACCACCAGGTACACCGCGACGGACTGCACGCCCCGGCGGTGGTCGGCCTAC TTCGGGAGGTCCAGGCGACGCGGGGGGGGGTGAGGGGATGCATGACTTTGTGATTTCTTTGAAGGCAACGCGCTT

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FIGURE 2M Filing Date: September

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 $\verb|TTTCCACGGCTTTCTGCCGCAGCTCCTTCAGCCGTGCGACGGTTTTTTCCTTGCCCGAGAGGATCTGGTAGTGCGGTTTG|\\$ $\tt CTCGACCTGCCAGGTCACGTCGGGACGAATCGAGGGGAGAAGGGACCTCAGCTTTTTCAGCTTGCCCGGGGCTTCAATGACTCGACCTTGCCCGGGGCTTCAATGACTCGACCTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTTTTCAGCCTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTTCAATGACTTGCCCGGGGCTCCTCAATGACTTGCCCTGCGCGCTTCAATGACTTGCCCTGCGCTTCAATGACTTGCCCTGCAATGACTTCAATGACTAATGACTTCAATGACTAATGACTTCAATGACTAATGACAATGACTAATGACTAATG$ GACGGTGCGTTGTTGCAGTTTTCGGGGCAACTTTCCGCGCATCGGCGAAAAAATATCCGTTGCCGATCAAATCGGACACA ACTTACCGATTCCTCAAATGCGGTAATCTTGTCCGTGTGGCTGCTGCAACCATCTACGGTAATCGTGGCAACTGGGTCGT TGTTGCTGCTCCTGGGCAAACCCTTTCAACCAGGACGCCCGCATCGCAGGATGACTGTAGGGGCAGTCGAACACCCGTAG TATCGGTCGCTCTTTTGACACACTGCACCTCGTACTGGTCGAGATTTCCGATTCGGAAGCCCTTGCCACCAGAGACTTC ACGAACGGGCGGCCAAAATTAAGGATGCTGGTCTATCAGCTTTTGCCGCCATAACTGTTCATTGCGGTTGCTCCAGTCGCTGGAATGCTTGTCGAGGCTGCGGGCGGCGAAGAGAGGGTTCTTGCCACCTGCAACTTCACGAGTGGGCGCGAAAAATTAAG ACCGGCGTTTCACCGTCGCGTCGGCAATGCCTTGGGCCATCCTGATGAAGGATGCGCGATCTTCTTCCTCCATAAGCGCC ATGCACTCTAGAACTGATATCTCGTCGGCGCTGAGGAGCTGCCTGGTCAACGGCTCATCGCGATCCCGAAATGAGCAATG ${ t TGAGCCTGCTTGGTCATCTTTGCTGTTCATGGCGGAGTTTCCTGCGGGGGCTTTGTCGAAGCTGCGGGTGGCAAAAAGT$ GGTACTTGECACCCGCAGCTTCACGAATGGGCGGCCAAAAATTAAGCCGCCTGCTACATGGGGATGTCGTCGTAGAGGC GCTGTCGTAGTCCTGCGGATTGCGCATCTTGCTGAGCAGGTTGCTGCGGGACGTTCCGAGACTGTTGATGCTGGGTTG GCAACAGGGTGACCTCGGCCAGGCGATGCGGAAGGATGGAAATGCGCGAGGCTTCGACCTTCAGCGCCTGGACTTCTTCG $\tt CCTGACTCTTTGTCCGGCCAGCGGTCCATAATGGCCCTGCCTTCGACCTTGACGCGCATACCTTTCGTGAACAGTTCGGC$ GAAGCGCTGGGCATCCTGATGCCACCATTCGACGCTGCACCAGAAGCCGCCGCGATCCTTGTAGCCACCTTGGCCATCGG GAATCGAGTTGTCGAACATCACGTTCAGTCGCAGCAACTGCCGCGGGGGATTGTTGCCGTTGGGGAAGCTGCGGTGCTCC GCAGTCGGCCCATGAACTCGGCCTCGGCCTGGCCCATCTTTTCCGCGCACTCGGCGGCCTGCTTGCCGATGGAGTGGATC AGGCTGATCTGCATGTTGAGGGTGATGCGCTGCAGCTCCATCTCGTAGAGGTCTTGCAGCAGGTATTCCGGGGTCTTGTC CGGATGTGCGCTGCTCGATGAGTCGGGTGGGCAGTAGAGTGAAGGGTGGGCGACGAACCTGGGCCAGCAGTCCCTGGGCA AGTTCAAGCAATCCCTGCTCCATGGCTTCGCACTGTTCCGCCAACTGGGCCAGCTCCCTATTACCTTTAAAAGGCTTTAA AAGGCCTTTTAGTGAGGCACTGTGTTGCAGCGCCTGGAAGGCAGTTTGTTGCAGTGGGCGGAAGGCACTTTGTTCCAGAG CGCCTTGCTGGTCCTTATCGAGCTGCCGCATTCCGATCAGTCCTCGAGTTCGACACGGTCAGCGTCATCATCGGCATCAC AACTTCTCGTACATCTTCCGCGCGGCTTCGGCGCGAGCATTGTTTGCGGCGAAGTCGTCGCGAGTGGCGCCCGAGAACTG GTAGCTCTGGGCCAGACCAAACAGGCTTCGCAGCACCGACGCACCTTCGTCGAGCCAGACCTCCATGTCGCGGCGACCGA AGAGGGTTGGAGATGAACAACGGGACCTTGACCGGTGTAACGGACAGGTTCTCGGAGATATCGAGGGTCGCGGGCAGCTT ${\tt GGCCATGACGTCATCCAGTCGGTCGATGGCCTCGAGTGCGGCTTGGCAGCTCTCGACTTTCTCTTCGATCTGAACCA}$ GATACATCTCAACCGTAATGGTCAACACGGTTACTGAATACCCGAACACGATCAGCATTAACAACAGCCTGAGTTCTCGG AGTTCCTCGTGAGTGGTGATGCCTCGCTTTGGCGAAAGTGTTTCGGCCCGAAACACCCATCTTGCCGCCGATACCGAAGTG $\tt CCCGACCGAGACTTTCTCATGAATCATCACCCCGCTCGGATGGCACGCTCGATCCGTGCCTGGGCCGAATGAGGTCCTTG$ AGCCGGCTGAGGACCTCGCTCCCTGTCCGGGTATCCCCCCGGGGCTGGACCTGAGGCTGTGTAGGCGCTATGGGGCTTGA ${\tt TGGTGCCGGAGCACGAATGGGGCGTTCCGTTGCGGGGATGGTTCGCTCAGCCGGTTCTTCCGGAGCCCAAGAAGCGTTGA}$ ACTTGCCCTGGACTGCACGCTGGATGAGCGTCATGAGGTAGCCGAACGGATTGCTGACTGTTCCGCCGGCACAACGGTGC AATCTTGTTTGTATGTATACGTACTATATGAGTTCGGCATCCGAACCAAGGGCGTACTCGGCGGATTCTGTCGGGGGTTCG TAAATCCGACAGAGTTCGGATGCCGAACTCTGCCGCTGGATCCGCTTCGAGCTGACTATCGATAGCCCATTGCTGGTGGT TCAAGCGTCCCTCGAGCTTCTCCAGATGGGTAGGGAGGCGGCGACCCACGTCCGGATCATCCCTGAACTCCCGCCAGATG $\tt ATCTGCCCGATTTCGCGTATGGCTCGGTTGCCGTGACCGGTGGATTGGCTCAGCAACTGCATGTAGTCGGTGTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTAGTCGGTGTCCAGCTCCAGCTCCAGCTAGTCGGTGTCCAGCTCAGCTCCAGCTCAG$ CAAGGCTTCGGCTGGAGAGACAGGCTCGTCGTGAAGGATGTAAACGTTGCCCTGGACCTGTCCGTTGAGGTCGTTGCGCA GGCGTCGGCCGAGGCTGAGCCAGCGGGTCAGACGAAGGACCGTGAGTGCCTTGGCGATGGTTTCGCGCGAGGCGATCTTG GAAAACTTGCCAGCAGTTCCGCTCCAGCGGAGTAAGACGCTTATCCAGGAGGAGGCGCCGTGGAACGGTTTCATGAGGAT GACTGAACCAGGTTCAGTAGTTGTTGACGTTCTGTCTCAGCGTTCACCTGCGTTGTTGCGGATGGGGCAGAGTGGGGCAG

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FIGURE 2N

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GTGTGAGCTGACGCTAGCGAGGTAAAGAGTGGATTGGGACTTTTGCAGGCCCGCCTGGCTCTGGCTCGATTTGCCAGACG GATAGAGCCCGTCTTTCAACCAGCTCTGGATGAGAGACCAAACAATGGCGAGGCTGATGAATTCTGGACTGTCTTGTTCG ATTCCGGCGTTGATTTCCTCTGTGAGGATCATCGCGATGTCCAGCAACTCCATGCTGTCTTCAAGGCGGACCTGATTTTC CTGCATCAGGTGCTCCCAGCGGAACCATATCTGGCGCTCGATCTGTTCATCGAGCTGCCGCCAGCGACCGCGGCGGCGGCGGCGGT GGATCTCCAGCATCAAGCGCTTGGTGGCGGTGTCCTCCGGCGACAGACCGAAAAAGCTCTGGATCATCGTTGTGGTGGCT GATGTTCACTCTGACATCTACCCAGGAAACCGGGGTATTGGTCAGGATGCTCATGACGGCAGGCTGTTGGAGCTGAGCCA GAATCTCCGGCCGCAGCCCCATCTCGGCACAACGCCTGAGCTGGCCGTTGCGCAGGTGGTTGAGCACCTGCGTCAGGACC GGCGGCCGGCGGCAGCTCAAGGTCAACCAGGCGTCGGGCAAGACGAATGATCCGGGAACAGTTTCACCAGGGCTTCGTCAT TGAGACGGCCTGCCTGGCAGGATGGCTTGTCACTTGTGGTGGGTTGGCCCAGCAGCAACTGAGCGAGGCCAGCTGAGAAC TGGAATTCACCCAGTGCATCGCGGCAGGTCTGTTGATCGTGAGTGTTCAGAACGACTTGGACCTGCCCGCTGACCGCTTG AAGCAGCGTCATGAGGTGCAGCGCTGAATCAGTAATCTCATGGTCTTCATTGGGCTCGCGATACGTGTAACCCACACCGC CCTGAATCCTGACGATCTCGCCTGGGGCGCCGACATGCAGAGCGATCTCTTCAGCCAGATCAGCGATGTGCTGTCGCAGG ATCTCGGGGGTATCGATCGACCGCTCGATGTACCAGAGATCGGTGATCGGGTGCAGGCCACCGACTTGCACTGGGATTGC TCGATACCGGGCTCACGATATGGCCTGCCAAGACCGCCGCACGCTCCTCATCGGGCAATTGCTTTTGTTGGACAGGTGGT GGCGGAGCCGGCGGGGGGGGGGTTACCCGGGTTGCTCCTTGTCCTGGACGTTTGGGGGATCTGCGGCGGGGCTCTGTGT TTGTGCTTGTCCAGTAGACGACGCAGCAGGGTTTTCCTGCCCAATTGGTGGGAGTTGAGGTGGTGCGGCAGGTGTGGGCA GGTCGACCAGAGTGCCGCGGCGTTGCTCCTGCTGCCCGTTGGTAATCTCGAGCAGGATTTGGTCATAACGCAGGCCCAGG . GGGCGCTTCATTTGGTCGATGAGTTCGTCCTGGAAACGCTCGAAAATGAATTCGTCAGGGCTACTGTCGAAGATTGCCAGGGTGTCCTGGAACAGCATTTCGAAGTCAACCCCTTCACCAGCGTATAGACGTGCCCAGCAGGAGGATGCCGACTTTCTGA GTGACAGGAGTTTCTCGATTTGCGGTTTACCGAGCCCTGAATACAGCATCACAGGAATCGCCGGCGCCCAATACCTCAATA GTGTCTAACATCTTACTGATATGGGATTGAGATACAGGGTAGCCGTCCGCTTTTAGCCGACGTGCCAACTCGCGCTGGGA AATGCTTTCACCGCCGTTCTCTTGTTCGTAAAGAAATTTCGCCTTCTGCACCCCAACCGCGCGCTCGATGAACTTGAGGT CGCCCTTCAGATCGTTCTCGGCCAAATGACCGGTCAGCGCGATGATTTCGCCGCGCTGCTTGTCCCAGGGCTTGAACAGG ${\tt CAGTCGAAGCTGAAATAGCGCTCGTCTCCGGTCTCTTTGTAGAGGTCGTTGAGAATTTCCAGGCGAGTGTTTCCGCCGTT}$ GCGAATGCGGTATTTGTCCTCTCCAGGGCGTCGAGTCACTGGTGGCGGCGTATCGAGGCCTCGATGTCGGATCGATTCTT TCAGCTCATCGTATTTCGGGTTTCGAGTGGTCCGGGGGGTTATCGTGCCAGGGGAGGACGTCGTGGAGTGTCAGCCTCATG GGCGTGTCGCTGATCGGGTCCGACAACTGCTCCAGAACCTTGGGCGGTGCGGTAAAACCAGGGGCAAGTAGCCGGTCTTT CAGATCTTGCGGGTTGATCTTGGCCATACTCATGCCTCCGCCACCTGAGGCGTGTTCGCCGCCGCCAGCTCAGCCTGCAG GCGCTGGTTCTTGGCGAAGAGTTCGTCGACCATTCGGTTTGCTCGCGCGAGTTCTTCTTCGAGCGCGTTGCTGCGCTCCA GTCGGTAGACGATCTCGCTGTTGGCCGAACGGTGGTTATCCGCGGCTTTTTGCTTTAGCTGATCGCGCAAGCCCAAGGGC ATACGGACAACGAACTTATCTTCGGTTTCTCGGGCCATGGTCATTCTCCAATTTGGGCCTTGCGCCCTTGAGCTGGTCG CGGAGTTGAGTGGGGAGGCTGATCTGCAGCGTGTCGCGCTCCTCGTACTCGATCCTGGAGCCCAGCAGGTGCGCCTCGAAGCTGATCGACAGGCCTTCGGCGGGCCGGTGAAGCGGCGGAACTGGTTGAGGGTGCGCTTGTCCGCCGGGATTT CCGGCGACAGGCCGTAGTCCTTGTTACGGATGTAGTCGTAGAACGCCCGCGGTTGCTGGTCGTCCATCAGTTCCGAAAGC GCGTCGAGGGTCATCGGCTCGCCGATGCGCGCCTGCGAGGTGGCGTAGTCGACCAGCGTCTCGGTCTTCTCGCGGGCCTG CTTCCTGGCAGCCGATGAAGTCGCGGAAATAGTCGGAGACCTTCCTCCCGCCCTTGCCCTTGATGAACGAGATGTACTGC TTCGACTGCTTGTTGTTGCGCCATTCGGAAATGTTGATCCGCGCGGCCAGGTGCAACTGGCCGAGGTCCAGGTGGCGCGA CGGGGTGACCTCCAGCGACTCGTTCACCGCCACGCCTTCGCTGTGGTGCAGCAGGGCGATCGCCAGGTAGTCGGTCATGC CTTGCTGGTAGTGGGCGAACAGGACGTGGCCGCCGGTGAAGAGATTGGACTCCTCCATCAGCTTTTGCAGGTGCTCGACC TGCGGAGCGGTCGACGCTCCAGCCTTCTGCTTGAGCGAAGGCCACCAGCCGGCGAACGCTTTCCCGGGCGCCGCGAAGGA AACTACGCATTCGTGGTCTCCTCGCTGTTGAGCTGCAGCCAGGTCTCCATCTCTGCAAGGGAGCGGGGAAGGCTATCGGT $\tt GGCGGCGGCATCCAGGAGACGTTTCACCAGCGCCTGAAGGCTGCGACGATCGCTCTGCCGGCTGCAGGCCAGGTCGTCAT$ GCGCGGAACGCAGCATGCGGACCTCTGTGCGCAGTTGAGTGCATACGTCGTCAGTTGCTACTGGTGCCGTTGACGCGACA GGTGACCGCGACCGTGTCCTGAGGCGGTTTTCCCACTCTTCCCTTGCCGAGAAGCGATGGCCACGACCTACACTCCA $\verb|ACCGCTGGTCCAGTAGCGCGAGTTTCCGCAGTCAGGGCAGGGCTGTGCGCCGCTGCCATCCAGGTGATAGCCGCAGTTCA||$ GACAGATCCACGAAGGACCTTCACGCAACTTGAGCTCAAGCATCAGCTCGACTTTCTGGAAGTGCTCGAGCGGCCGGTAG ${\tt GCTGTGACGTCAGGCATCGCGCGCTACCTCCTTGGGATTTCTACAGGACAGCGCCCCAGCGGCTCTCGATGCGCTTTTCGT}$ ACCTTGTCGCTCCAGGTGCAGGTCGCACGCTGCTTCTGAATGGTATTGGTCCAGAAACCGGCGCCATCGAACTTGACGAT GCACTGATAGGTCTGGGACGCCTTCATGACTCGGCCTCCTTGCTGAGTGCATCACCGACCTGAACGGCCACCAGTTCGGG GGAACACGGCGGTGAGGTGCTGGGAGTCCTGAGTGCCGCAGCAGAGGTGCGGCACCAGGCTCACTTTCAGCGAGCAGCTG AACAGGTGTCGCGGGATCCATACCGACCAGAGTAAGCCGAAAGCAATTGCCCCGGAGCGCGCGTAGTGACCACCAGAGT CCCGGCCTGGGTGGTCGAGATTTCGATGTACCCCAGTTCCTCCAGCTCACGAAGCTCTCGCTCCATCGAACTGGGTGCGA GCATGAACCACTGCCGAGTCGGTGAACGCGGCCGAGGCGTGGATACTCGGAAAGCGGGCTTCAGTGTTCATCAAAGACAG CCTCCAACTGATGGACGTCGTAGCTTCCGCAGCAGGGGCAGACCAACACCTCGGCTTCTCCTCTGGGGTGTTCTCGGCG GTTCATGCATGGGCTCCTTGCCAGGTCCCCGGCGCCCAGGTCGGCAAAGCGGGTCTGGTTGGCGATGAAGGCGGTGTGGAC GGTGCCGATCGGACCGTTGCGATACTTGCCGATGATGATTTCGGCGATGCCCTTGGCCTCGGTGTTGGGGTGGTAGACCT CGTCGCGGTACACGAACATGATCACGTCCGCGTCCTGCTCGATTGCGCCGCTCTCTCGTAGGTCCGCGCAGTTCGGTCGC TTGTTCGTCCGGTTCTCTAGGCCGCGATTTAGCTGGGATAGAGCTACGACGGGACAGTCCATCTCCTTGGCCAGCGCTTT

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CAGCGAGCGGGAGATTTCCGAGATCTCGGTGGCTCGATTCTCCAGGCCTGGGCAACTCATCAGTTGCAGGTAGTCGACCA TTGGCCCTTCATCAGCTTGCCCAGGTCCAGGTGGCCGAACAGGGGGGGCAAGCCTGAACAGCAACTGCTCTGCCGGCATCT CCATGCTGTACACCTGAACAGACTTCTGTTGGTCGCTCTGGAGCGCGGTGTCGACCAGGTTGAGGGCAAACGACGTTTTG TATCGACGAAATCGGCGTTGTGGTGGTCCTGGCCAAGGGCCGAACAGCTTCTGCTCAATCTCCTCCTGAACCTCAGAGGG TCTGGAAGGTCTTCGATCGCTTCCGACACAGTCACGACATCAAACGGAGCATCCTTCGCGGCCAACTCGCTGATGGCGGT GAAGATCAGCCGATGCTCATGCCGGAAGAAGTCCTCCTTCTGCAACTGATCGCCGACAATGTCCCATGCCGCGTTGTCCA ${\tt TTCGATGGTGGCAAAGAGGTGATTCCGCAGATCCTCAATCTTGTTCTTCATGCTCGACCTCCTGAATGGTGCGTTTGAGC}$ TGGTGCGCGTCCTCGCGGGGCAGCCCCTTCATGCCGCAGTTCCATGGGGTGTTTCCCTTCTTGAACCGAGTTGCGCTGC TCAGGGCCGATCCCTCGGCCCATGAACTTGAACGTCCAGCCGGCTGGCATCGCGTATGCCGCCAGGTAGTCGCAGCCGAA GCCTCGTTCGGCGTGGCCCCCTTGGCATTCGCCAGGGCCATCAGCTTCTCGACCTTGGCGAGGACTTTTTGCTTGTCCAT TACGCGCCCCCTTGCAGATGGTTGAGCCCTGCTCGGTGGCGGAGCGGTCCAGGCGCTCGATCTCGGCCAGCACTAGGGC ${\tt GCCGGCGCGTACCAGGTTCTCGCGCGCCGACTTAGGCTTCCACCACTCTTCGTCCCAGGGCCAGAACAGTGCAGAGCCAT}$ GCGCTAGCGTCGTTGCTGGTATCGAAACCTTCGACGGTGATCTGGCGCCGGCGCTCGGCCTGTACATCGAGCCAGGC $\tt CTGCGGAACAGGGGAGAGGTTCGAAGTTGGGTAAATTCGGTCTGTGGCCTGTCTTACCCGATCGACAATAGCCAGGGCTG$ $\tt CTACGTCGCCCAGTGCGACCTCCAGGGCGGGCGAGCAGGTTGGCCATCAAGAACTGCTCACGCTCGTCCGCGTGGTTTTTT$ GTGAACCTGGCAGTCCAGGCATTCAATGGCACAGTTCCAGGCATCGGTGTCGAGCAGCTCGGGTTCCAGCATTCGAATGT TAGCTTGGGAGGAGCCGGCGACGAGCAGGTCGGCCAGGTCCGGATAGTTCGGGATGGGTCCAGAAGCCGAACTGATCGCGC TTGGGCGAACTCGGCCAGGTGATCGATGGCAGTAGCTATGTTCCAGATCGCCCTGTTCATGTCCCGCTGGATCACTTGGA TCGAACTGGCATTGGCCGCGATGGCCAGTTGCGATTTCGTCTGCAACAGTAGGTCGTGGGCGATTTGGAGCAGTGCGTTC TGCAGGGACTGTCCACAGGCACGCTGCTGAGCGCGAACCGGAGCGACCAGGCCCTGCAACATCGCAGCACCTTCAGCCTC GATTTGCAGATTCTCGGAAGCACCGGCGGCAGCGCCTGCTTTGGCCATGTAGCCTTGCACGTAGGCGTCGAACTGGGTCT CGGCGATCAAGCTCAGTAGGAGGTTGTTGCGGTTCTGGAGGTTCATATGAGGCCCTCCGGAGCCGATTGCAGAGCGTCTG TCCAGAGCCGAAGGGTTTCCTGCTCCTCGCTGGTCAGAGCGATCTGTGCGGTGCAGTCAGCGACCTTCTGCTTGATGACG $\tt CGCAGGCGCTCCTCGACTTCACTGCCATCGTCGTACGCGATTTCGTTAGTCAGATGGCTAATGAAGTCACATCGCAGGCT$ TTGAGTGGAGCTGGTGCGTGGAGTACAGGTGATCGAACACCCTGGCCCGGTTGTAGATCAACGCGATCTGCAGGATTTCC AGCCGATCTTCGAGCGTATTTCCCGGAAGCGGGTAGTTCGAGGCGACCAGTTGCTTGGCCAGGCGCTCACGTAGCTCGCG CCGCTTCTTGGCTTTTTTCTCGTAGCGATCACGCTTTTCCTTCGCATGCTCGATCTGCTTGTTCACCGAGTCGAGCAAGC GCGCTGCGTCTTGTAGGAGCTGCTTTTGTTCGAAGCTCAAGTAGCAACCCAGCTTCCCGAACAGGTCGATACCGCCACCA GTCAGCTTGCGTATTTCTCGCGTAGCGCCGGTCAATTTGGCCTGCTGGCTCCGAAGGTCGGCGGCGCTGCCGAACTTGTT AGTGCTGCAACCGCCTCCCGGCGTCAGCGCCAGGAAGCGGTCAGTCCACTCGGGAAAGACCTCGATGGCCAGGTTTCGAA TGATTTCCAGCGCGGGCGCTGATGTGCGATTGGAGGGTTGCCGCGTTTCGAGGCGGTGCGCTGGTAGCCCGCGCGATGCT GACGCTCATAGGGGCGTAGGCCGTCGAGCATTTGCATGGTGCCGCGGTTGAACTCACGGGCGGTAAGCATGTTGGGTTGG ${\tt CAGGTCGTAGCCTTCTTCAGAGCGGGCATCAGGTTCGCCAGGCGTAGCCGGCCATCGGGCGCCTGGAGCAGTAGGTTGT}$ TGAGCTGATTGTTCTGGTCGTTGGAAATCACGACGTCCAGATTGGGGGATAATCGTCCTGGAGATGATCCTCGCCGGGTCC GACGGGGTCCAGATCGATGAGGAGGGTTCGTATGCCTGCATCGGCGCAAAATGCACCGAGGTTGGCGGCGGTGGTGGATT TTCCTACACCACCCTTGGTGGATACAACCGAAGTCGCTTTCGCATTCATGTCTACAGCCTCTAATGTGGGGTCATTAGAG ${\tt GCTGCTAAACAGACTCGTTGTAACGGGAGTGGAAACCCTTCCTAGAGAAACCTACGACCAGTTGTCTTTTAACCAATTGG}$

FIGURE 20

FIGURE 2P

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TCGTAGGTTCGAATCCTACACGACCCACCA

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FIGURE 3 RL024

DNA sequence (SEQ ID NO: 3)

GTGGCGCTGACCGGTAATCCCCTCCTGAAATTGCTGGTCGTCCCCGTCGTGATCGGCGCCATCCTGATCGGCGTGAGCAT GATGGGCAAGAAGAAGTGCGCAGTCACAAGGCGCCGCAACCCCGACGGTAACGTCGGAAGAAGCGGCAACCCTGGGCA TCGACGGCGACACGCCCGCCGACACTACGCACCATCGTGGCGGAAAGCCGGCAGCTCAAGGACCAGATCAGCAAGGTG ATCCAGGAGAATGACTCGCTCAAAGCCGCCAATGAGAACCTGCAGGGCCGCCTGCGCAACATCGATCAGAACATCGAGCA GAAGCTCAACAACACCGCCCAGGAACTGCAGCAACAGCAGGAAAACCGTAGCCAGACGATCCTGGACCAGGTACAGAAAC GGCTCGAGAACCTAACCCACATTCCCGAGGCCGGTGACACCGACCTGCCCGTAGGATTCGGCGTGCGACCAAAGGATGGC CAGCACTTTCAGGGAGCGGGCTCGTCTTCATCGGATATCGTCTGGATCGAGCCCCAGGACGCCCGCGCGGTTGATGCCAA TGGCCAGCCGCTGGCCGCCGGCTCCACCCACCCAACCGAGCGGATTCAGCTTCCCGACCTCCTTCGGCAATGCGGTCGATC GCGGACAGAACGCGCTGGAGCGGATCGATGACGGGCTGCACCCCGTCGGCCAACAGCGATCTGACCTGGAAAACCGCAAG CTCGTCCGTAAGACCTACACGCTGCCGCAGAACTCGACGCTCATGGGCTCGGTGGCCATGTTTGCGCTGATCGGTCGTGT CAACAACAACCAGACCGCCAGCCGACCAGAAAACCATCCAGGGCGGCCTCGGCTGGATCAGCGACCCCTACGGCATCC -ATTGCCAAGCTCCTGGACGCCGACGAGAACAACACCAGTACCGTCTTCAGCGGCAACGGCACCAGCTTCGGGACGACCAGCTCCAGCTCGACGACGACGACCAGCTCCAG AACCAACAGCAACTCGGCCCTCAACAGCATCCTCTCCGGCGGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACG GGGAGGCCTTCGCCGCCGTCTACGTGCAGCCAGGTGCGCGGGTCGCAGTGCATCTCGATCAGCAACTGGCGATCGACTAT GAACTCAAGGGCCGCAAGGTCGATTACAGCTCTGGAGCCGCTCATGCAACAGCAGACTTGGACTAA

Protein sequence (SEQ ID NO: 127)

VALTGNPLLKLLVVPVVIGAILIGVSMMGKKESAQSQGAATPTVTSEEAATLGIDGDTPADTLRTIVAESRQLKDQISKV IQENDSLKAANENLQGRLRNIDQNIEQKLNNTAQELQQQQENRSQTILDQVQKRLENLTHIPEAGDTDLPVGFGVRPKDG QHFQGAGSSSSDIVWIEPQDARAVDANGQPLAAGSTTQPSGFSFFTSFGNAVDRGQNALERIDDGLHPVGQQRSDLENRK LVRKTYTLPQNSTLMGSVAMFALIGRVPVDGTVNDPYPFKILIGPDNLTANGIELPDVAGAVASGTASGDWTLSCVRGQI RSLTFVFNDGTVRTFPAPAEEVNDNQSNNNQTASADQKTIQGGLGWISDPYGIPCIAGDRRSNAKEYLGNQSLLTAAGAG IAKLLDADENNTSTVFSGNGTSFGTTGTNSNSALNSILSGGVSDIRQWMNKLYGEAFAAVYVQPGARVAVHLDQQLAIDY ELKGRKVDYSSGAAHATADLD.

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FIGURE 4
RL025

DNA sequence (SEQ ID NO: 4)

Protein sequence (SEQ ID NO: 128)

MIRKSTGSLLLMLALPTLAHAVEILRWERIPLAIPLTVGQERIVFVDRNVRVGVPRDLQGKLRVQSTGGALYLLANEPIP PARLRLQDATNGEQMLIDIAATEATADQQPREPVRIVAGEPVDPHYGQSREAQPSAAAKQTEHAEAPKAVPRETPVPVVLTRYAAQMLYAPLRTVEPVDGVGQVRVKRQLDLTTLLPSLPITATALGAWRLDDYYITAVKLQNASAQHLALDPRDLMGNFVAATFQHPYLGPRGDASDTTTVYLVTRGRGLADALLPSSISQIDPKGGRRGADR.

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FIGURE 5

RL026 : DNA sequence (SEQ ID NO:5)

Protein sequence (SEQ ID NO: 129)

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MSFRKHTAQQQAHINTFRFITGFLCMVIVVLAYCVWEARKDLWIHIPPDLRSGSTRLWWDIPPESVYAFGLYIFQQVQRWPKDGEVDYKGNLFRYAAYLTPSCKVFLEKDFEFRRNAGELRGRERTTSEIPGRGIGESNGRVIQHSINDWTVNLDMDSTEYYAGEKIKRALARYPLHVIRADVDPETNPFGLQWDCYSDTPQRIELEEPAAPTKREGGL.

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FIGURE 6

RL027

DNA sequence: (SEQ ID NO: 6)

ATGCCCGAAGAACATCTGTTTCAGGATGGAACCCTCAGCTTCCTGCCGACCC
GTTTGAACCGGCAACCGGTAGTCATCGG
CGGCCTGACCGCAGACGAAATGTGGATCACGGTCTTCACCAGCGGAGCAGCC
GGGTTCGTTCTTGGCATCCCGGCTGCCT
TGGTCGCAGGTAACGCTGCCTGCATTCCACTGGGCGCGCTGCTGGTCGGCGC
CCTCGGCCTAGGTATCGGCAGCCGCGTC
CTGCGGCGGATGAAGCGGGGGCGGCCCGATACCTGGTTCTACCGCCAGGTGG
AGATGGCCCTCTCGCTGCGCTTCCCGT
CTTCGGCAACCGTCGCCTGGTTACGCGCTCCGGCGCCTGGACCAGTCGACGC
ACGGAGTCCCCATGA

Protein sequence: (SEQ ID NO: 130)

MPEEHLFQDGTLSFLPTRLNRQPVVIGGLTADEMWITVFTSGAAGFVLGIPAALV AGNAACIPLGALLVGALGLGIGSRV LRRMKRGRPDTWFYRQVEMALSLRFPVFGNRRLVTRSGAWTSRRTESP.

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FIGURE 7

RL028

DNA sequence: (SEQ ID NO: 7)

Protein sequence: (SEQ ID NO: 131)

MLKLTLQKLSALCQSLAAITLALPGIALAALPKPEAPSRGEGSGIMQTIQNFGYDGAMLLALLICAAVFLGVAWHTYGTY HAIHDGKKKWSDLGAGVAVGVGLLILIIYLVTKATAIM

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FIGURE 8

RL029

DNA sequence: (SEQ ID NO:8)

Protein sequence: (SEQ ID NO: 132)

 $\verb| MSMSGAQTSAFQAAAGFPPSAGEGLFIGAAMTFLLLWSAWAMYSTWRGWATNNLRQRHRWRFRDPGSWSSSASPLSSSSADPYGDTHAETHPPETVRPLPEPGRHHFGAPRYRLGCTPQTRGT.$

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FIGURE 9

RL030

DNA sequence: (SEQ ID NO: 9)

Protein sequence (SEQ ID NO: 133)

 ${\tt LICTRFAVNTPHPSLRRSCLAVLACSALVAQGAFAASASEQANLEVMIRQLNALEDTARRSAQGADEPGQRFYFDYPRLAADLQRIRQGLQDYMTPSRAQPRDPSDLSGNYTLRGGPMP$

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FIGURE 10

RL031

DNA sequence: (SEQ ID NO: 10)

ATGAGCATAAAACAGCCCTTCGAATACCATGTCGAGAACATCGTCATTCCCTACAAAACCCTCACCAAGGGCGTCGCGAT GTTCAAACACAAAGAAGACACCTTGGAACCCGACGACCACGCCTTGCTCAACCCTCTGCGCTGGGCCGAGGTCGTGCGTC TGGGCCAGGAAGGCTGGGAGCTGGTGAGCGTTCAGCCACTCATGCGGGGCGTAACCGAGATCGGTAATCAAAACGCCCAA GGCTGGGCTTGGGGCGTCGCTCTGCCCGTCAGCTACCTGCTGTTTTTCAAGCGCGCAACCTCATAA

Protein sequence: (SEQ ID NO: 134)

 ${\tt MSIKQPFEYHVENIVIPYKTLTKGVAMFKHKEDTLEPDDHALLNPLRWAEVVRLGQEGWELVSVQPLMRGVTEIGNQNAQGWAWGVALPVSYLLFFKRATS.}$

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FIGURE 11

RL032

DNA sequence: (SEQ ID NO: 11)

Protein sequence: (SEQ ID NO: 135)

MLRNISIGVLLAMAAMLGSYGVAAATLRCGSAIVSEGDLIDDVLRKCGNPDSRKIEGPAVDGSGYIVRGAATVENWVYGPRNGWYQKLRFVDGRLVQIKGSMD

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FIGURE 12

RLO33

DNA sequence: (SEQ ID NO: 12)

Protein sequence: (SEQ ID NO: 136)

MKLILDFDGRLLNPSNMLEALSKAGKNTSISISNAQALNIETLLKATTTAENTKNLSTTFNGAELTANNLQQVINSAGSL TRVSTIAAQAININTLLSAISTAGNSKNFSAEFNGAQLSSDNLLRAVNAAGTNTSISVNTAQAANITALLQTIHAAGDTK TFSAEFNGAQLTSNNIQQALDAAGTRTSISVNTAQAVNISTLLALINSAKDTKKFSADFNGAQLTADNLQQAISAAASGT NISVNTAQAANISTLLQAINIAGNTKKFSANFNGAQLTSNNIQQALRATGSNTSISMNSAQSANQSTLLELLDIASSSKQ FQANYNGGMSNPNNLQQIVFPCRRQYNRVYFRRTRPTNRKYPYPYIICRMRLIAVDENTPSTAIP.

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FIGURE 13

RLO34

DNA sequence: (SEQ ID NO: 13)

GTGCAGTGGACTCACGAACAGTCACCGATCATCCAGTCGAAGGCACCGAAGATCCTGGTGCGAGCCTTCGCAGGCACTGG CAAAACTACCACCTGGTGGGCTTTGCCAGGTCGAACCCTACCCTGAGAATCCTCTATCTCTGCTACAACAGCTCGGTGG AGAAAGCCGCGAAGGGCAAGTTTCCCCGCAACGTAGTGTGCAAGACCGCCCACAGTCTGGCTCATGCGGTGTACGGCATT CAGTACGCCCACAAGAAGACGAAGAACCTGCGACTGACCGATATCGCCCGCGGACTCGATACCCAAGACTGGGAGTTGGT ACGTGACGTGCTGGCCACGCTGAACAACTACATGGCCAGCGCGGCGGGAACTCGGCCGACCGCACTTCCCGCGCTTCC ATGGTCGATCTCCAGGACACCGGCATGCTGATGCCCCTTGACGGCTACCTGAAGCTGTATCAACTGAGCAAGCCCGATTT GAGCCAGCGCTTCGACTGCATGCTCCTGGACGAGGGGGCAGGACATCAACCCAGTGATCGCGGACATTGCCCATTGGCAGC GCATCAGAATGGCTATCGTCGGCGATCCCCATCAGCAGCTCTACCGGTTCAGGGGCGCAGAAGATGCCCTGAACAGCGAC TGGATGGCCGGCGGAGGAGCACTACCTGACCCAGAGCTGGCGATTCGGCCCCGCGATCGCACACGTGGCCAACATCAT TTCCTCACCGCACTTTCATTCACCGCACCGTTATCGGCGTCATCGAGAATGCCCTGCAGCTGGTCCGCAATCATCCGGAG $\tt CTGACCCTTGACGATGAGCTGGACGCAACAATCACCCTGACCACCGCACACAGGGCCAAGGGGCTGGAATGGGATTTCGT$ TTGCCTGTACGACGACTTCAACGCGGACCCGCTGGCCCCCGACACCCGACCCAGGCAAGCGCGACGATGAGTTGAACCTGA TCTACGTCGCAGTGACCCGCGGATGAAGATCCTTGCCATCAACAGCCTGGTGCTGTCGATCATGCAGCGGTACGTGGAC GACAGAAAACTGAAGGAGCAGATAGCTAGCTGTAAAAAATGA

Protein sequence: (SEQ ID NO: 137)

VQWTHEQSPIIQSKAPKILVRAFAGTGKTTTLVGFARSNPTLRILYLCYNSSVEKAAKGKFPRNVVCKTAHSLAHAVYGI QYAHKKTKNLRLTDIARGLDTQDWELVRDVLATLNNYMASADAELGRPHFPRFRDKAFLTSAQERFLKQGLDMARVVWRR MVDLQDTGMLMPLDGYLKLYQLSKPDLSQRFDCMLLDEGQDINPVIADIAHVARIRMIVGDPHQQLYRFRGAEDALNSD WMAGAEEHYLTQSWRFGPAIAHVANIILSYKGETRKLQGLGPQTLVKKSLPPDLPHRTFIHRTVIGVIENALQLVRNHPE PKFHWVGGIDSYSLRDLEDLYAFSRGLRQNVQNKKLLRDYRDYTQYVEIAEISQDGEMLRSIKIISTYPDLPARILELRS LTLDDELDATITLTTAHKAKGLEWDFVCLYDDFNADPLAPDTDPGKRDDELNLIYVAVTRAMKILAINSLVLSIMQRYVD DRKLKEQIASCKK.

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FIGURE 14

RLO35

DNA sequence: (SEQ ID NO: 14)

Protein sequence: (SEQ ID NO: 138)

MFGSLIGAIIVEWVCLYFFWPDAGWKHAQAMFEYELŚWLSQGLLHSVVVQEPGRTATWLAQLAYDWLFVKTGMVDWMTNM TTIAQARPRSPLDVRYLTAHGVSTLQNYGLAALYTVLTFVVRLVILVMTEPLFVMAAFTGLVDGLVRRDLRKFGAGRESS YLYHKARGSIIPLAVVPWTLYLAIPISINPLLILLPCAALLGVAVCITASTFKKYL.

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FIGURE 15

RL036

DNA sequence: (SEQ ID NO: 15)

ATGAAGTTGAAGAATTTCTTACAGCCTTTTGATAGCGGTTTCTCCACTCCGAGTGCTGCGCTCAAGCTGCTCCGCATGCT CGGTGCCCTTGATGTTGTGCGTGCTATGCAGCCTGATATTCAGTGTGAGCATGGTTTTAAACCATCAGGTGTCCCTCA $\tt GTCGGCAAGCTATGAATGTGGCTATGTACGAAGCGCAGCTTTATTTCGAGCAGCGCGAGGCGTTGCTCAATCACTTGAGC$ GGCAATGTCGTGCCCTTGGCCGCGGGTAGAGCGCTCGTCAACGAAGCGCCGAACAATGTGAGCATCCTGCCGTTGAGTGA CGGAGGGCGAGGTCTGCTATTGACCGCTCGCACGCTCGGTGATCTCCGGGAAAAGCGGCTGGCACTGATGTATCTGGTCG $\tt ATACCGACAAAGGCCCTCTGGTTTACCGGCTTACCGCCGATGGTAGGCCCTCGGCAGCGATATCCAGCACGATAACCAAA$ TGCGCCGGAATGATGCCGGAAACTACATGCTGCTGGATCAGCATGGGCAGGTCGTACTCGCTACGGACGCAGAGGCGCTG GGGAGCGGTGCGTCGCGGACGCTTTTGCGTGGAGACGGCTTCGGTTTCATCGGTGCTGGCCCACTGCCGCAGCATATGGT TTGATAGAGCCCGCAAAGCGACGCCTTGAAGCATTGAAGGAGAGCGAAGCCTTTTCCCGTGCAGTTATCCAGGCCGCGCC CGTCGCGCTGTGCGTGCTGCGTGCCGACGCCGCAGTGGTCCTGGAAAATCCCCAGGCGCGCCAATGGCTGGGTGATA GCGAGGCGATTGCCCACGACGCGCCGAGATGGATTTCCCAGGCGTTCGCAGGAGGTGTGAAGTGTTCTGGAGAAGAACTG GAAACCGAGGCAGGGCTACATCTCATCTCAATTACACGCCCACCCGCTATAACGGTGAAGACGTATTGTTCTGCGCCTT CAGTGAAATCAGTGCACGCAAGCGGATGGAGGCGGAACTGGCTCGCGCAAAATCCCTGGCGGATGCTGCCAATGAAGCCA CGTACCGAGCTGAGTCGGCAGCCGGTTACCTAAAGGCAATCCAGCATTCCTCGTCGACCCTGCTGCAACTGATCAG AAGAGGTCGTGCAGTCGTTCACCGGTGCCGCGCGCGCGCCAGGCCAAGGGGCTTGCAGTTGTATACCTGCCTCTCTGCGGAGCTGCCG TGGCTATGTCAACGTCCACCTGAAGGCCAGCGTGGTCGATGCCGAATGTGTGATGCTGACCTGGCAGGTCAACGATACCG GCATGGGGATCAACGTCGAGGATCAGCCGCGTCTGTTCGAACCGTTCTACCAGATACGCCGCTCCGAGCATCCGGTCGCA GTTGGGCAGCAGCTTTAGCCTCAGGCTTCCGCTTGAGCGGATCGCGATGCAGGCTGAGCCGCAGGACCTAGCCGGGTGCG GTCGCGACGCCGAGGTCGCTGGACGAGGCGGACGCGACCTCGCTGGTCAAAGTGTTACTGCTGGAGGGGGCGCCGAT GTTCGAAGCATGGCCAGGATGCCGGGTGGAGCTTTCCCCTCAGGGTGATATGGAGCCGCAGGCACAGGGCCGCGACTGGC CCGATACGGCTGGCTCCGTTGCGCAATCTAGGTCTCCGCGTCCTAGTGGTGGAGGATAACGCGATCAACCAGTTGATCTT GAGGGACCAGATGGAAGCGCTGGGCTGCAGCGTGGAGCTGCTCTTCGATGGTCGCGAGGCGTTGCTGCACTGCCAGACGG CCTGCTTCGACGTGGTGCTCACCGATATCAACATGCCGAACATGAACGGATACGAGCTAACCGCGGAGCTACGGCGCCAA GGGTTCCGGCAGCCGATCATCGGCGCGACGGTGAACGCCATGCGTGAGGAGCGCGAGCGCTGCATGTCCGCCGGGATGAA CGATTGCCTGGTCAAACCGGTGGATCTGAATGCCCTTCAGAACTGCTTGATTAATATTCTCAAGGTGGATCGATGA

Protein sequence: (SEQ ID NO: 139)

MKLKNFLQPFDSGFSTPSAALKLLRMLGGALMLCVLCSLIFSVSMVLNHQVSLSRQAMNVAMYEAQLYFEQREALLNHLS GNVVPLAAGRALVNEAPNNVSILPLSDGGRGLLLTARTLGDLREKRLALMYLVDTDKGPLVYRLTADGRPSAAISSTITK EVYRALLATPSAPVHWVTDGGTPQRLYLFESLGDEPGEGWLGLEILGEDLDSMLRRNDAGNYMLLDQHGQVVLATDAEAL GSGASRTLLRGDGFGFIGAGPLPQHMVLFQHVGSSSWDLIYHIGIGRLLLALWLPLLLASALALAVGILLHWLVRSIERR LIEPAKRRLEALKESEAFSRAVIQAAPVALCVLRRADAAVVLENPQARQWLGDSEAIAHDAPRWISQAFAGGVKCSGEEL ETEAGLHLHNYTPTRYNGEDVLFCAFSEISARKRMEAELARAKSLADAANEAKTLFLATMSHEIRTPLYGMLGTLELLG RTELSRQQAGYLKAIQHSSSTLLQLISDVLDVSKIEAGQLDLECVEFSPLELTEEVVQSFTGAAQAKGLQLYTCLSAELP LRMRGAAASIRQILNNLLSNAVKFTDNGYVNVHLKASVVDAECVMLTWQVNDTGMGINVEDQPRLFEPFYQIRRSEHPVA GTGLGLSISQRLAQLMNGSLKLVSELGLGSSFSLRLPLERIAMQAEPQDLAGCAVQVLAPVRDLTECLCGWISRWGGRAM VATPRSLDEADATSLLVKVLLLEGAPMFEAMPGCRVELSPQGDMEPQAQGRDWLLGLNNLNGLHRALGLAHGRLADPSTP PIRLAPLRNLGLRVLVVEDNAINQLILRDQMEALGCSVELLFDGREALHCQTACFDVVLTDINMPNMNGYELTAELRRQ GFRQPIIGATVNAMREERERCMSAGMNDCLVKPVDLNALQNCLINILKVDR.

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FIGURE 16

RL037

DNA sequence: (SEQ ID NO: 16)

Protein sequence: (SEQ ID NO: 140)

MSWKSYRVLVVEDQPFQREYLLNLFRERGVQYLVGAGDGAEALRCLKQDRFDLILSDLMMPGMDGIQMILQLPYLKHRPK LALMSSSSQRMMLSASRVAQSLGLSVIDLLPKPTLPKAIGQLLEHLERCLRQKLEPETDETPHGRTALLDALHNEQLVTW FQAKKSLHTGRIVGAEALIRWSHPQHGLLLPSCFMSDVDATGLHEALLWRVLEQTLNAQESWRRAGYEIPVSVNLPPHLL DNQELPDRLYEYVGARGACTSSLCFELTESSVTTLSSNYYAGACRLRMKGFGLAQDDFGQGYSSFYNLVTTPFTELKIDR SLVQGCVEDNGLNAAVISCIELGHRLNLDVVAEGVETCEELNLLRRLGCDRAQGFLISKAVSAREFERQLREDGPSLLV.

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FIGURE 17

RL038

DNA sequence: (SEQ ID NO: 17)

GTGAAGTCTGCTAGTGCCTTGGAGCACGACAACCATTTTGCTCAAATGGACAACCCTCTCGCAGAGCCTGAGCATCGG CTTGATCTGTGTGGTGGTGCTGACCGTATTGCTGTTCAGCATCTGTTACTGGTCGCTGGGGAGATTGTTTCAGGAGGAGG AGGACAAAGTCTCCTTCCACTTCACCCGTATGATGGATGTTATACGGGAGCATGAGGTATTTCTTGGGCGCATCGCTCGA AAAAGCGACAAGACCACCCAGAAGTACGACTATGACGTGGTGCCTTTGCAGCGGCACTTGTTGGCAAAGGAAAACGGATT AGCGGTCTATGAGGGACGGGAGTTTTCCTTTGCTATGCCATTTCTACTGGCTACCAAGCACGCGTTGAGCGCCGATTCCT CAGTTACTGATCTTTGATCTTTCCGGCAGCACCCGCCTGGCAGTGCCGTCGATTCCCTCCACAGCGCAGCGTGACAGGTT TCCATTGGATACGCGTGATCGCTATCGCGACTCGGCGCTGGAGATGTTGGGAGTCGCCCGGGTTGATCTGCCGGAAACA CTCTGGTGGCACGACCGACCCGAACCATCTGATCATCGCTGCGAGCCTTGATCTCAGGCGAATCAATGACTTCGAACA GTTGGTTGAGCGCCCGGCATTCGATTCGTACAGCCTGGTATCGCCGGATGGCGAGGTATTGCTCGGCGGCCCCTGCGA GCGGTCTACCGAACCGACTACGGCAATTTCTTTCGCCACTCCCGGTGGCTGGTGGCAGGTCTGCTGCTGACCCCGGCGCT -GETECTGGCGGGTTGGCTCGGGATGCGTTGGTAGACCAGCAGCGTCGTCAACCCGGTGGATCGGGCGCACCGGCAACTGG TGGAGAGCGACACTTCAGCCGGACGCTGATACAGACCGCGCCGCTGGCTCTGGTGGTGCTGACCCAGGATGACCAGCAA TTTCGATGCGCGTGGGCAGGTACCAGGAGACATCTGTATCCAGGTCGGTGGGCGCTATTTGCAGACCGCCTTCGCGGCGA CCCGCTATGCCGGCACCGAGGCGGTACTGTGCGTATTCAACGACATCACGGTCCACTGCGAGGCGGAGACCGCGCTGTCC AATGCGAAGCGAGCAGCGGATGCCGCCAGCCAGGCCAAGACCCTGTTCCTGGCCCGCATGAGCCATGAAATCCGTACTCC TCCAGAGTTCGTCTGCGACGCTCATGCAACTGATTAGCGATGTGCTGCATGTCTCGAAGATCGAAGCGGGGCAGATGGCT CTGACCCTGGCCGCCTTCAATCCGCTGGACCTAGTGCGGGAAGTGCTTGGCAACTTTGCCGCCAGCGCCATGGCCAAGGA CCTGCAGTTCTATGCCTGCATCGACACCGAAGTGCCGGCGCAACTGATCGGTGACGTGACGCGGATTCGCCAGGTGCTCA ATAACTTGGTGAATAACGCGCTGAAGTTCACCGATATCGGACGGGTGGTCCTGCGGGTGAAGTTGCTCTCCCGCAATGAT GGTCGAGCCCTGTTGCAGTGGCAGGTCGCCGACACCGGTATCGGTATCGCACACGAACAGCAGGAGCGCTTGTTCGAGGC GTTCTACCAGGTTTCGGGAGCGCACCATGCCGGCGCACGGGGCTAGGACTGTCGATCTGCTGGCGATCTGGCGGAAATGA TGGGCGGTCACCTGCGAATGGTCAGCGAGACAGGGCTCGGCAGCAGCTTCAGCCTGGTGCTCGAGTTGCCCGAGGACGAA CAGTCCGGGCTGGCTTGCCGGCCGGGGCTCTTGAAATCCGCTTGCGTCCATGTGCGCTCGCCCGTGCGGGAGCTAGCCGA CAGCGTAGGGGCGTGGAAAGCCTGGGGCTGCAAGGTCAGCAGCGGCGGCGGCGCCCTCCGAGCTGGAGACTTGTG TGCTTCTGGAGCTGCTGCCGATGGCGGCCGGGCCTGCTTCTTCGCCCTGGCCAGGCCCCGGGTGCGCGCGTCCATGGAT GCGCCTTGCCAGCCGGAGCTGCGTGAGGACGGCTGGCGTGTCGGCCTGCACAACCTGGCGGGAATCGGCCAGGCCCTGGC ${\tt GCAGGCTCTGGGTGGCGATATCCCCGAGCAAACGCCGGCAAATGCCTGCGCCCGCTCGGGGAGACTCGACCTGGAAGTGC}$ TGGTCGCCGAGGACAACCCAGTCAACCAGGCGCTGCTTCGCGAGCAACTGGAAGAGCTGGGTTGTCGCGTGAGCCTTGCC GGCGATGGGCGGCAGGCCCTGCAGCTGTTCGACAGTGGTCGCTTCGACCTCCTGCTCAGCGACGTCAACATGCCGAACAT GACCGGCTACGAACTGACCCAGGCGCTGCGCGAACGAGGCGAGACGCTGCCGATCATCGGCGTGACCGCCAACGCCCTGC GAGAAGAGGGCGAGCGCTGCCGGGCAGTGGGAATGAACAGTTGGCTGGTGAAGCCGATCACTCTGCATACCTTGCATGAA CGAACGCTGGTGGTGATGTCTCAGGGCGCCGAGGAAGGCCTGCTGGAGTCGCGCCTTGAATGTTCCGCCGTGGAGATTGG ${\tt CGAGGTGCTCGTTCATATCGAGCAGGCGCTGGAGTTTGTGAGAAAGACGGGCTGA}$

Protein sequence: (SEQ ID NO: 141)

VKSASALEHDNKLLLKWTTLSQSLSIGLICVVVLTVLLFSICYWSLGRLFQEEEDKVSFHFTRMMDVIREHEVFLGRIAR KSDKTTQKYDYDVVPLQRHLLAKENGLAVYEGREFSFAMPFLLATKHALSADSSGDPFSLGVLLANFYGSFWSVSAYPAP QLLIFDLSGSTRLAVPSIPSTAQRDRLSGSYPMIVERILARLRTRPVGEDAQRVHWIRADRYRDSALEMLGVARVDLPET LWWHDEPNHLIIAASLLDLRRINDFEQLVERPAFDSYSLVSPDGEVLLGAAPATGLRDGLNLTRQGVAVQLLSQPENGWL AVYRTDYGNFFRHSRWLVAGLLLTPALLLAGWLGWRWYTSSVVNPVHRAHRQLVESDTFSRTLIQTAPVALVVLTQDDQG LVTCNHLAAQWLGGPTEILGLTSNWKLFDARGQVPGDICIQVGGRYLQTAFAATRYAGTEAVLCVFNDITVHCEAETALS NAKRAADAASQAKTLFLARMSHEIRTPLYGVLGTLELLDLTTLHERQRAYLRTIQSSSATLMQLISDVLDVSKIEAGQMA LTLAAFNPLDLVREVLGNFAASAMAKDLQFYACIDTEVPAQLIGDVTRIRQVLNNLVNNALKFTDIGRVVLRVKLLSRND GRALLQWQVADTGIGIAHEQQERLFEAFYQVSGAHHAGGTGLGLSICWHLAEMMGGHLRMVSETGLGSSFSLVLELPEDE QSGLACRFGLLKSACVHVRSPVRELADSVGAWLKAWGCKVSSGEAAPSELETCVLLELLPMAAGPASSPWPGPRVRASMD APCQPELREDGWRVGLHNLAGIGQALAQALGGDIPEQTPANACARSGRLDLEVLVAEDNPVNQALLREQLEELGCRVSLA GDGRQALQFDSGRFDLLLSDVNMPNMTGYELTQALRERGETLPIGVTANALREEGERCRAVGMNSWLVKPITLHTLHE LLSEFARAGVVLPAQARDLGPPAQLDDGLSPQVPERMRALFLETMGKDLEAARQAIRRNDPKGLQQDLHRMAGSLAVMRA RTLVVMCQGAEEGLLESRLECSAVEIGEVLVHIEQALEFVRKTG.

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FIGURE 18

RL039

DNA sequence: (SEQ ID NO: 18)

Protein sequence: (SEQ ID NO: 142)

MRPGSIVGIRTQEKPMSKLKIVLADDHPIVRMGVCDMLERDGRFEVVGEASTPSELVEVCRQSEPHIAITDYSMPGDERY GDGLKLIDYLLRNFPRTKVLIFTMVGNRLILDSLYDHGVSGVVLKSGELDELLLALDVVKQNRVYRGANMLDPTSVLANR DEVESRFARLSMKEFEVLRHFVSGSNVCDIARLLKRSVKTVSTQKVSAMRKLEVNSDQALMTFCVHANLFH.

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FIGURE 19

RL040

DNA sequence: (SEQ ID NO: 19)

Protein sequence: (SEQ ID NO: 143)

VSSKI LLQGALLGLAMLAVLDARAGVTAERTRAI IAEGHRETSLLLVNQNAYPVIVQTWIDDGAPNSTPQSARAPIMPLP PVFRLEPGQQRSLRLLRTGQALPGDRESLYWLNLYEIPPQATGLLAEGQSRLTVTLRTQMKVIYRPRPLARGAEEAPHQL RFERRGETLQMENPTPYFISLAGAELGGHTRLAAAELLPPFSRRVLALRQALPGGQAEVRFSWIDDGGNLQQGRSLLH

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FIGURE 20

RL041

DNA sequence: (SEQ ID NO: 20)

ATGAAAACATCCCTGCGCGTCCTGCCCCTCGCCCCCGCGCTGCTCGCCTCGTCTAGCTGGGCGACCTGCTACAAGGTCAC GGCGGTAGGCAACGCCACGACTACCTCCAACACCCAGATACGTCCCGGTGAAGGCTCTGCCGGCACCTGGGCCGGAGCCT GCGATACCTGCAACGGTTCCCTCGGTCTACCGAGCGTGATCAACGTCAGCGACGCCAGCTTCCAGCCCGACGGTAGCTTG ATCGCCAGCTCGGTGGCGCCGCTCAGCCAATACGGCGACAGCGCCGGCTACGACCCAGAGCGCGTGTTCTTCCGCTGTGC GGGCAGTATTTCACCGATGTCTGGCGCGAGCGTCTGCTCGGCGGGCTCGATATCGACTCGCGAGGCTTTCAACTGGTCAA GGCGAAGAACCTCAGCGCGGTACGCGCGGAACTGTTCCGCGCTCCGCTGGAGTTCATCCGCTACTACTCGCCGACTACCC GCCAGCCATAACGCCAACTACCTCGGCTGGCACTACAACTGGCCGGGCGCCATCGGCCTGTACAACGACGTGACGCTCAA GCGCTATCCCACCTGTTCCGTAACCAACGTCACGCCCCACGTTGTGTTCCCGTCGATTTCCCTCAGTGAGATTAATGCCG GCGCGAACCGTGAGATGCCCTTCGAGGTGGCCTTCAAGTGCCAAACGGGAGTGATCAACAGCACCGCCTCCAGCGGTACT $\neg \circ$ CTACCTAGTTTCCGACCGGCTACGGCCAGCCTGGTATGGCCCAAGGCGTGGGTATCCGCTTGCTGCGCGACGGCAGTGCGA ${\tt TGAACCTGCTGGTAAGCGAGGATTCCGCGATGGGCAGCAATGCCGAAACACGGGGCTGGTATCCAGTGATCGGCAACGCC}$ TCGAACAAGACTGGCGAAGCGGGAGGCATCAGCCAGTACAGCGAGACCTTCCGTGCGCGCCTGGAAAAACTCACCGTTGG

Protein sequence: (SEQ ID NO: 144)

MKTSLRVLPLLLALLASSSWATCYKVTAVGNATTTSNTQIRPGEGSAGTWAGACDTCNGSLGLPSVINVSDASFQPDGSL IASSVAPLSQYGDSAGYDPERVFFRCAPEDDVYEMFSTNADDLYSGWYLGGDSAGNSIGLQSAYRTAWPNVLLRLTHVET GQYFTDVWRERLLGGLDIDSRGFQLVKAKNLSAVRAELFRAPLEFIRYYSPTTASRLYAYTQPAGYIAIKGPGLAYPNVG ASHNANYLGWHYNWPGAIGLYNDVTLKRYPTCSVTNVTPHVVFPSISLSEINAGANREMPFEVAFKCQTGVINSTASSGT ALGIRASAGAQAASAALGLRNANGGLSYLVSDRYGQPGMAQGVGIRLLRDGSAMNLLVSEDSAMGSNAETRGWYPVIGNA SNKTGEAGGISQYSETFRARLEKLTVGSMPSVTPGRVEASAQVVIRVQ

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FIGURE 21

RL042

DNA sequence: (SEQ ID NO: 21)

 ${\tt GGCCAATGGAGGCGCAGTATCGTTTCGACGACAGCCTGTTGATGGGCTCGGGGCCTCGCCGGCGGGACCCTAGAACGCT}$ TCAACCGGGCCAACCAGGTGGACCCGGAACCTACCATGTCGATGTCTATCTCAACGGCAGCTACGCCAGTCGCACCAGG ATCGAGTTCCGCCCCGGGCCGGCGTCAAACCCTGCTTCGGCGAACGCTTCTTGCGCCGGACGCTGGGCGTCCGCCC CGCCTCTGAGGCCGGCGTGCAAGCGCCTGGAGATTGCCTGGGGCTGGAAGAACGCCTGCCAGGCTCGACCTTCAATCTCG ACACCGCCCTTCTGCGCCTCGATCTCTCGGTGCCCCAGGCCCTGCTGGATATCAAGCCACGCGGCTACGTGGGTCCCGAC GAGTGGGACGCTGGCAGTAGCATGGGCTTCGTCAACTACGACGCCAGCTTCTATCGCTCGAGCTTCGACGGAGTAGGCCG $\tt CAACGGCGACTCGGACTATGGCTACCTGGGGCTGAGCGGGGGCATCAATTTCGGCCTGTGGCGCCTGCGCCACCAGTCACACCAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAAGTCACAAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTCACAGTCA$ ACTACAGCTACTCCAGCTATGCGGGAAACACCCGCAGCGACTGGAACAGCATCCGCACCTATGCCCAGCGCGCGGTGCCA GGCCTGCGCAACTGACCCTGGGCGAGAGCTTCACCGAGGGCAATCTGTTCGGCAGCCTGGGTTATCGCGGCGTGCG TATGGCACCGCCTACGACGGCGATCTGGATGTCCAAGTGATTGAGGCCGACGGCAGCGTCTCGCGCTTTTCCGTGCCCTT TTCCGCGGTTCCGGAATCCATGGGCCCGGGCATCTCGCGCTACAGCGCCACCCTCGGCCAAGCGCGCCAGTATGGCGAGCG GCAACGACCTGTTCGGCGACTTCACCTATCAGCGCGGCCTGACCAACTCGCTAACCGCCAACCTCGGCTCGCGCCTGGCC GAGGACTATCTGGCGCTGCTCGGCGGAGGCGTGCTCGCCCACGCCCTACGGAGCCTTCGGCTTCAACAGCATCTTTTCCCA TGCCACGGTGGAGAACGGCCAGCGCAAGCAGGGCTGGCGTGTCGGTCTGAACTACAGCCGGACCTTCCAGCCGACCCAGA GATGAGCACAACGACTCCTGGAACTCCAGCAGCTACAAGCAACGCAACCAGTTCACCCTGCTGGTCAACCAGGGCCTGGG GGGCTACGGCAACCTGTATCTGTCCGGAGCCACCAGCGACTACTACGACGGCAAGAGCCGCGACACCCAGTTGCAGTTCG GACGACTACGACCCGTCACTGCCGCCAATACAACCTGCGGCACGGCAGCGAACGTAGCAACACCTTAACCCTGACACT GCAGCTACCAGACGGGCCTCAACGGCACCCTCGACGAAGACCGCAGCCTGAGCTACGCGATTGCCGCCGGGCGCGACAGC GACAACCACGGCAGCGATTTCAACGGCAGTCTGCAGAAACAGACCTCGGTGGCGACGCTGAACGCCGGCTATGCCGAGAA TCGGCGACACTTTCGCCCTGGTCGAGGCCAAGGGCCCCAGCGGAGCTGGCGTACGCGGTGGTCAGGGCGCGCGTCAAC AGAGGCCGAGCTGCTGGAGACCGAGCGCAAGATCGCGCCCATACGCCGGCGCCCGTGCATGTGAAGTTCCGCACACTGA AGGCGGTGATCCGCCTGCAGGGCACCTGCACGCCCGTCTCGGAGGCACCATGA

Protein sequence: (SEQ ID NO: 145)

MFCHVEARRTGKLPLALGGLALAFAGLANGEAQYRFDDSLLMGSGLAGGTLERFNRANQVDPGTYHVDVYLNGSYASRTR IEFRPRAGGVKPCFGERFLRRTLGVRPASEAGVQAPGDCLGLEERLPGSTFNLDTALLRLDLSVPQALLDIKPRGYVGPD EWDAGSSMGFVNYDASFYRSSFDGVGGNGDSDYGYLGLSGGINFGLWRLRHQSNYSYSSYAGNTRSDWNSIRTYAQRAVP GLRSELTLGESFTEGNLFGSLGYRGVRLASDDRMLADSQRRYAPQVRGTANSNARVVISQNGKKVHESAVAPGPFVINDL YGTAYDGDLDVQVIEADGSVSRFSVPFSAVPESMRPGISRYSATLGQARQYGDGNDLFGDFTYQRGLTNSLTANLGSRLA EDYLALLGGGVLATPYGAFGFNSIFSHATVENGQRKQWRVGLNYSRTFQPTQTTLTLAGYRYSTEGYRDLGDALSARHA DEHNDSWNSSSYKQRNQFTLLVNQGLGGYGNLYLSGATSDYYDGKSRDTQLQFGYSNTWRQLSYNLAYSRQTTWYRDLN DDYDPSLPPQYNLRHGSERSNTLTLTLTLSMPLGSSSQAPNLSAMASRRSGDSRGSSYQTGLNGTLDEDRSLSYAIAAGRDS DNHGSDFNGSLQKQTSVATLNAGYAENSSYRQLNTGLRGAAVLHRGGLTLGPYVGDTFALVEAKGASGAGVRGQGARVN GNGYAVVPSLSPYRYNPVSLDPQGMGEEAELLETERKIAPYAGAAVHVKFRTLTCHPLLIQAQLADGSALPLGANVLDSQ GVNIGMVGQGGQVYARAEGDKGRLRVQWSERPGDACLLDYDLDTGPRQAIEPGQAVIRLQGTCTPVSEAP

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FIGURE 22

RL043

DNA sequence: (SEQ ID NO: 22)

Protein sequence: (SEQ ID NO: 146)

MNTFPLPPLRAATLALALLI PAI PAQSSVVI I GTRVI YPGDAREKTVQMI NQDAFPNVI QAWI DNDDPSSTPETANAPFL VSPAVTRI APGSGQTLRLLYTGLPLPEDRESLFHLNVLQI PPRDLAKAERNQMLLMQRSRLKLFYRPAALLGGSEQLVEQ LHFSLVQASGNWRVRVDNPSGYYASFAGAMLS I GERRWRLLSSMVPPKGQAEWAAERPSPLAPGPVQLNALLINDYGARM EVQHVLPR.

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FIGURE 23

RL044

DNA sequence: (SEQ ID NO: 23)

Protein sequence: (SEQ ID NO: 147)

MKPQSTALTIAAFLALPGIAAAANTITFHGEVTDQTCSAVVDGRTDPTVILDTVPVSALDGAVGKPAGETSFTLQLTGCA
APAADAEEHFSVMFQAVNPTSAGNLTNTASAGATGVALQLLTAPGGSEVNLAGGSAVAAGDIVLAGGETSTSYDYAVRYI
----SEATTVTPGPVLGSVTYTLRYE

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FIGURE 24

RL045

DNA sequence: (SEQ ID NO: 24)

GTCCCGAGGCCTTTGAAAGCGCCTCG

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FIGURE 25

RL046

DNA sequence: (SEQ ID NO: 25)

ATGGCTGAAGTCACTCAACGAGCAGAGCAGCAACAAGAGAGCCAGAAGACCCTTCTCGGCACCATCATCAGTACGCCCTT CCAATTTCTCGGCGTGATGTTCGGGTCGCTGATCGGCGCAATCATCGTGGAGTGGGTTTGCCTGTATTTCTTCTGGCCTG CTGGATGACCAACATGACTACCATCGCGCAGGCCGGGCCACGGAGCCCGCTGGACGTTCGCTATCTCACCGCCCAGGGTG CGGCCGGGAGTCCAGCTACCTCTACCACAAGGCGCGCGGCAGCATCATTCCGCTAGCGGTCGTCCCTTGGACGCTCTACC TGGCAATTCCCATCAACATCAATCCCCTGCTCATCCTGTTGCCCTGCGCCGCACTGCTCGGCGTAGCGGTGTGCATCACA GCATCCACCTTCAAAAAGTACCTATAG

Protein sequence: (SEQ ID NO: 148)

MAEVTQRAEQQQESQKTLLGTIISTPFQFLGVMFGSLIGAIIVEWVCLYFFWPDAGWKHAQAMFEYELSWLSQGLLHSVV VQEPGRTATWLAQLAYDWLFVKTGMVDWMTNMTTIAQAGPRSPLDVRYLTAQGVSTLQNYGLAALYTVLTFVVRLVILVM TIPLFVMAAFTGLVDGLVRRDLRKFGAGRESSYLYHKARGSIIPLAVVPWTLYLAIPININPLLILLPCAALLGVAVCIT ASTFKKYL.

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FIGURE 26

RL047

DNA sequence: (SEQ ID NO: 26)

CGCGCTCTGCATCGTCGCCGTGGACGTTCTCCCTCACTCCGCTGTTCGGCATCGTGGCCGCGCTGTGCTTCGCCTGGC TGGGTATCGTGCGGCTGAAGCAGGCCGGCGTGGTGCTCCGCTACCGGCGGAACATTCGCCGACTGCCGAAGTACACGATG ACCAGCGCCGAGATGCCGGTCAGCAACGAACACCTGTTCATCGGTAAAGGATTTCGCTGGACGCAGAAGCATACGCAGCG AGCAGCTCGAGTTCGCCCCTTCCCCCTGAAGCTGGTCGCCAAAGCCACTGCCTGGGACGTGGCCTGGAACCCCGCACGG CCGCTGCCGCCCGTGGGCGGTTTGCCTCGGCTCCATGGCATCGAGCCGCGCGAACAGGACGTAGGCCTGCAACTGGGCGA TTCGCCGCACTCACTGCCGGGTACGACGCCGGCGGGTGAAGATGGGCCGGCGGACCCAGACGGTTCACCACGGCTATCGG TATGTACGTGGAATGCGAACGTGCCGGCCGCCTGGACGAGTTCTACGTGTTCCACCTCGGTCATCCTGACCTGTCGGCAC GCTACAACGCCGTCGGCCGGTTCGGTCGGATCTCCGAGGTCGCCACCCGCGTCGCCGGCCAGCTCTCCGGCGAGGGCAAC AGCGCGGCGTTCCGCGAGTTCGCCTGGCGGTTCGTCAACATCATCGCCCGCGCGCTGCACGCGTGGGTATCCGGCCTGA CTACCAGCAGATCCTCCGGCACGTCGTGAACATCGATGCGTTGTTCGTCGAATATGCGCAGAAATACATCAGCGAGCACC ATCCCAGGGCCTGGGACACCATCATCCAGATCGAGGGCAAGCTCAACGACAAGAACATCCCGTTCAACATGAAAGGACGG CCCCTGCGGGTCGTAGCCATCGACCAGTACCTGACACAGAAACGCATCGCCGACCCGGTCATGGAAGGCTTGAAGAGCGC CGTGCGCTACGACAAGACCTACTTCGACAAGATCGTGGCCTCGCTGCTGCCGCTACTGGAGAAACTCACTACCGGGCGGA TCTCGGAGCTTCTTTCGCCCAACTACGCGGACCTCAACGATCCGCGGCCGATCTTCGACTGGATGCAGGTCATCCGCAAA $\tt CGCGCCGTGGTCTACGTCGGCCTCGACGCACTATCGGATACCGAGGTCGCCGCGCGGTGGGCAACTCCATGTTCAGCGACTCCGAGGTCGCCGCGCGGGGGCAACTCCATGTTCAGCGACGCGAGGTCGCCGCGCGGGGGCAACTCCATGTTCAGCGAACTCAGAACTCAACTCAGAACTCAGAACTCAA$ CCTGGTCTCGGTAGCGGGTCACATCTACAAGCATGGTGTCGATGACGGCCTGCCCGGCTCGCCAGCGGCAAGGTCC GGCGTGCAGGTGACGCCTACACCCAGACCATGAGCGACATCGAGGCCAAGATCGGCTCCCGCGCGAAGGCCGGTCAGAT CATCGGCAACTTCAACAACCTGTTCATGCTGCGGGTGCGCGAGACCGCCACGGCCGAACTCCTTACCAATCAGCTCCCCA GTTCGCGCTACTCGAGGGCGGCAATCTCTGGAAGATCCGAATGCCGCTGCCGGCGGTCGCCCCCGACGAGGTGATGCCGA AAAGCCTGCAGGAGCTGGCCGGTATGCGCAAGGGCCAGGCCGCCAACAGCGAGTGGTGGGAGGCGCCGGGATACTCC GCCCTGCAGGATGGTCTGCCCCAGGACCTGGTCGACGATTTCCGTCACCTCGGCACCGGTGAGGATGCCGCCTGA

Protein sequence: (SEQ ID NO: 149)

MAGQYPLEALLRPAVELYTTVCFTAAALCIVAPWTFSLTPLFGIVAALCFAWLGIVRLKQAGVVLRYRRNIRRLPKYTM
TSAEMPVSNEHLFIGKGFRWTQKHTQRLADTYLPQFASYVEPSPLYERARRLEKQLEFAPFPLKLVAKATAWDVAWNPAR
PLPPVGGLPRLHGIEPREQDVGLQLGERVGHTLVLGTTRVGKTRLAELFITQDIRRTHCRVRRRRVKMGRRTQTVHHGYR
RRRAEEQPDYEVVIVFDPKGDADLLKRMYVECERAGRLDEFYVFHLGHPDLSARYNAVGRFGRISEVATRVAGQLSGEGN
SAAFREFAWRFVNIIARALHALGIRPDYQQILRHVVNIDALFVEYAQKYISEHDPRAWDTIIQIEGKLNDKNIPFNMKGR
PLRVVAIDQYLTQKRIADPVMEGLKSAVRYDKTYFDKIVASLLPLLEKLTTGRISELLSPNYADLNDPRPIFDWMQVIRK
RAVVYVGLDALSDTEVAAAVGNSMFSDLVSVAGHIYKHGVDDGLPGSLASGKVRINLHADEFNELIGDEFIPMVNKAGGA
GVQVTAYTQTMSDIEAKIGSRAKAGQIIGNFNNLFMLRVRETATAELLTNQLPKVQIYTSTPASGANDAINNNKKVAFTS
SSHDQVQMTSVPMLEPAHIIGLPKGQAFALLEGGNLWKIRMPLPAVAPDEVMPKSLQELAAGMRKGQAANSEWWEAPGYS
ALQDGLPQDLVDDFRHLGTGEDAA

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FIGURE 27

RL048

DNA sequence: (SEQ ID NO: 27)

ATGACTACTCATCTGATCACCCTAGTCATCAAGCAGCCGAGCGACCGCCAGCCCAACTCATGTACCAGGAGTTGCT
CGGACTGATCTCACGCTACGGCGTGAGGTGACGTCCAAGGCCTTGGAGGACGACTCGACCCTCTGCGAGCTGCTGGTGC
AGATGCTGCCTGATCATGAGGTAGAGCAAGCCAGGAAACAGGTGCTCGAACTTCATGCCAAGGGCCGCCTGCAGGCGCCG
GCAAGCCTGAAGGTGTAA

Protein sequence: (SEQ ID NO: 150)

 $\verb|MTTHLITLVIKQPSDAQARQLMYQELLGLISRYGGEVTSKALEDESTLCELLVQMLPDHEVEQARKQVLELHAKGRLQAP| ASLKV$

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FIGURE 28

RL049

DNA sequence: (SEQ ID NO: 28)

Protein sequence: (SEQ ID NO: 151)

MKKFLATLAFCTAFATQAWAAGLIVVEDLGGASALPYYQGLDPQPSASAPGPGDLGVRGSGAFPVRSARLSPGRVQGRAI NAPGLQLLFLVGDDTLSRTWLKERGDELRDLQAVGLAVNVASEARLTEIRAWGKGLQILPAPADDLVDRLGLQHYPALIT STAIQQ.

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FIGURE 29

RL050

DNA sequence (SEQ ID NO: 29)

ATGGCAACGTCTGTAGTTCGAGCCCTCCAGTTGGCCACCTGCTGGTCCTGGTCAACATCGCTCAGGCCGCCGTGGATCC
ACCGCCGGCGTACAAGCAAATCGCCCTGCCCAAAGGGGTTCCGGCCGAGGTGCTCTACTCGGTCGCGCTGACCGAGAGCA
AGGTCCTGCTGCGCGCGCAATACGTTCCCTGGCCCTGGACATTGAACGTCGCCGGGAAATCTTACTACTACCGCGCCCGC
ACCGCCGCCTGCACAGCGCTACTCGCGGGATCAACCTCTACGGGGCCAAGAGCGTCGATTCCGGCCCAGGTCAA
CATCGGCTGGAACGGACATCGTTTCTCCAGCCCCTGCAGTCCCTTACAAGAACCTGGACCGCCACCTCCGACA
CCTGATCGAGCAGCGGGACGCCCTGTATGCATCCCCCCGGGAAGACCGGTGGACTGGATCCAAGTTCCCGGCCGCTAC
CACCGCCCGCCGGCGGCGCCCTGCCGCCAAATACCGTAGGACCGGTTTCCCGCCACCTTAGCCAAGTTCTCGGCGTCAA
CCTACTGGTGACCAATCCATGA

Protein sequence (SEQ ID NO: 152)

MATSVVRALQLATLLVLVNIAQAAVDPPPAYKQIALPKGVPAEVLYSVALTESKVLLRGEYVPWPWTLNVAGKSYYYATR TAACTALLAAINLYGAKSVDSGLGQVNIGWNGHRFSSPCESLDPYKNLDATSDILIEQRDALYASAPGRPVDWIQVAGRY HRPAGGAPAAKYRRTVSRHLSQVLGVNLLVTNP

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FIGURE 30A

RL051

DNA sequence: (SEQ ID NO: 30)

Protein sequence: (SEQ ID NO: 153)

MIRTVSLLSGLMLLLSYPAAGQEAAASREASSQLSGSQLGTLKQQTSQSDLAQEWGLNQQEWTRYQTLMQGPRGAYSPGI
DPLTALGIEARSAEERRRYADLQVQAERRRVEKELAYQRAYDEAFARAYPGEGVIRLTESSTANPSGTPNMSPALQSSGR
LATFVQDNCTACIQRVRDLQHAEKEFDLYFVGSQNDAERVRRWAILAGIDPKKVRSKQITLNHDEGRWMALGLGGALPAL
VQEVNGRWQRL.

RL052

DNA sequence: (SEQ ID NO: 31)

Protein sequence: (SEQ ID NO: 154)

MKRPSPASMILGLCLTAMAGLLSYQQYQLVQLRSGVDSAAEKASLEAILARLSRVDERLDAVDGQHLVSNEDFRSGQQAL SNRIDAAQAFAKQASDAVENLAQTTASAGDLLVLKATVETLDGSVRTLQEKQAKAPPLIVPAPKRPIPAKPKPKPKPMEP PPFSILGVEYRGGERFLSVAPPGSTQLSQIYLIRRGDAVAGTTWRLTDLDDGTAHFDVAGTSRSVRIQP.

RL053

DNA sequence: (SEQ ID NO: 32)

ATGCCGCGCCGCTTGATCCTCTCGGTCACGGAGCGGGATATCCTAT TGCACTGCCGGTAAGCCGAATGACCTCACTGAC
TACTCCACCTCAACGAGTCCGCCCCATCGTCGATCCGCCAGCGACGCGATGCCAATCACTTGGTTTTTTCGGTGCAG
GTCAGCCTGCTGTGCTATCCAGCCTTCAGCCCTGATGCGCGACGAAGAGCCCCCGAG

RL054

DNA sequence: (SEQ ID NO: 33)

ATGGCCGAAGCTATCAGAAAGGATGCAATGATGACAAAACTCTACTTTGATCTTCTGAACTCGCCTGCCGAGGCTCATTC
GTCGATACAAAAGTCTTTATCTGTGCAGGCAATCTCCACAACTGTCCCAATACTGGAGTTTCCTTCGGAAAACCGTATACG
GTCGATACAAAAGTCTTTATCTGTGCAGGCAATCTCCACAACTGTCCCAATACTGGAGTTTCCTCCGGAAACCGTATACG
CCTATGCATCGTACATAAATGCATTAAGTATCGGTCAACGCATAGATCCTGCATTCACCCAGAGCTTAACGAGTGCCATA
TCCAACCTGGCAGGTCGCCCGATTGCAGTAAGCGACACTTTACCAAAAAATTCATGAAACCACACTGAGAACACCTGTTGA
GATGGGCGTTCGTCCTAATAGCATCACCTTTGAGGAGTATCAGGCCAATATGCAGTTCCTGTATGGACAGGAGAATAAAT
ACTGATTTCATCGCTCGTAATGAACTCGCTGCTGGGCAGAGAGCGAAAACCGTCGCAATAGTTCAGGGCCATATCACCAT
CGGGTACGGCTTCGATACCTTCGTGCATGAAGCGTCCGAGCTAAACTCTTTGAATCTTTGTTGTTCTACGCGACAAGAGG
TATTACCTGCATTGCAGCTATCAACGTCCGACCCAGGCTTCTGGAGCGTTATGCCTTGCTGGGACAAACTCACCGGT
GACGATGGGCTATTACTCTTTTAGTGCCAAAACGGTTGCGTTGTTCAACGCATAGCAACCAGTTTCCAAGAT
GAATGGGCTACCCCCAGCTATCAAAACGGTTGCGCTTGATCTATTATCAATATGGGCAGACTGGTAATTTTCCAAAAT
TTCAACAAGCTATAAATAGCCATGATTGGCCGGCAGCTCATCCATGCAACTTTAGAAACTGGTAATTTTCCAAAAT
TTCAACAAGCTATAAATAGCCATGGAAGGCGAGCCCAAGTATCTGCGCAATGATCATCACCAATGA

Protein sequence: (SEQ ID NO: 155)

MAEAIRKDAMMTKLYFDLLNSPAEAHSSIQKSLSVQAISTTVPILEFPSETVYAYASYINALSIGQRIDPAFTQSLTSAI SNLAGRPIAVSDIYQKIHETTLRTPVEMGVRPNSITFEEYQATINQQAINMVQDMQDGDKGEKVEALQANMQFLYGQEIN TDFIARNELAAGQRAKTVAIVQGHITIGYGFDTFVHEASELNSLNLVGSTRQKVLPALQLSTSDPGFWSVYALLGQSLTD DDGLLLFSAKARAVVQRIASNQFAGKWNGLPPAIKTVALDLYYQYGQTGNFPKFQQAINSHDWPAVIHELRNWNGVPNDP LQFITKRLEERAKYLAISFNYEQ.

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FIGURE 30B

RL055

DNA sequence: (SEQ ID NO: 34)

ATGAACACACAGTGAGCGAAACGCAACAGATCAATATTTACCAAAATCCGGGGCAGTCTATTTCCGGTCTCTACAAGGG ${\tt GCTGGCTAACCAGTGCTCTCCTGGCCAGCCATTTCCAGAGGTACAGCTTGTGGAGGCTTGGGATATCCCTCTCGTACTCC}$ ATCCGGAGTTTGTGCCTAACGGAGATGTCTCGAAAATCGATAAGGAGTACGGAACGATCCTTGCTGCTGAGTCAGCTCAG GTTATCCTGCTTCAACTCCAAATGGCTCAAGACAAGGCTAAGGCGTGCGGGGAGGTTACAGCCTTGATCAGTTCTGTCTC CTCCAATCTCAATACCATTAAGAGTCGTCATGGTGCTAATTATCTAAACCTGCTGAAACAATCACCGAACCGATACCCGA GAAGCTTTCTCAGCCTGAATATTGGCCTGCTTACAACAACATAGCCACTGGTATTCGTTATACAACCGGAGTGGCGATAA CGTTGGCCTATTGGGCCACGGTTTAG

Protein sequence: (SEO ID NO: 156)

mnntvsetqQiniyqnpgqsisglykglanqcspgqpfpevqlveawdiplvlhpefvpngdvskidkeygtilaaesaq VILLQLQMAQDKAKACGEVTALISSVSSNLNTIKSRHGANYLNLLKQSPNRYPTSVGVEIMSGGSPNQDSGIEVSYGASL GRLTQSQLQAMNLPASLKQLLTQGIGVKLSQPEYWPAYNNIATGIRYTTGVAITLAYWATV

RL056
DNA sequence: (SEQ ID NO: 35)

ATGACCCAAGCTGCGAAAATACCAGCAAATGAGTACTCATTGGGGGATGGAAGAGGGCTACATCAATATCTGGCCGGAAAA GGATGAGGCTCAGGCATTTCTTATCCATAATGATGGGCCTAATGGGGCTACATGCAGCCTTAAAGGCACTCTTAGAGATA ATAAAGGAGTGGTGCATTCGCCGTATTCCTCTGCTTCATGTTTGCTAAGTATCACCCAGACAGGGCTGCTGTCAGTAAGC GTCAAACGTGAGGAAAATTCGCCAAGCTGCTCTGCATGGTGCGGTCCTAGAGTTTGGTTTGAAGGAGCCTATAGCGTCCC GCCCAAGGGCTGCTACTATATGCAAATAAGGAAAAAACTCGACAAATGTTGGGTATGATTGAGAAAAAAAGAGCTTGATG ACACTTGCCATGATCAGTGCTGAAAAGGGAGAGATGCTCGCTGTTTGGAGTATGCCCATCGGGTGCAAAAGCAAATTCC $\tt TGTAAGAGATGACGGCCAACCGGCTGAAGACTTGCTCCCGGCGGAGCACGCTTTCGCTATGGAACAACGCGCCAAGGCTG$ ATGCTCTGTCTGAGCGATGCAGCGACGAGAAATAA

Protein sequence: (SEQ ID NO: 157)

MTQAAKIPANEYSLGDGRGYINIWPEKDEAQAFLIHNDGPNGATCSLKGTLRDNKGVVHSPYSSASCLLSITQTGLLSVS vkreenspscsawcgprvwfegaysvppkgcyymqirkktrqmlgmiekkeldaaralsnkllsdcatelaypakiyltn TLAMI SAEKGENARCLEYAHRVQKQI PVRDDGQPAEDLLPAEHAFAMEQRAKADALSERCSDEK

RL057

DNA sequence: (SEQ ID NO: 36)

CTGGTGCTGCTTGTATGCTCAGCAAGCCAGCCGCCGGTCTTTTCAGGGTAAGCGTACGGCCAATACACCTTTACTTA GGTTGA

Protein sequence: (SEQ ID NO: 158)

VLVERLPTDVEFAGELSLGLAGRCPQPQGSTCLSDKASLRPRYAQSLISSRYRAGAACMLLSKPAAGLFRVSVRPIHLYL

RL058

DNA sequence: (SEQ ID NO: 37)

ACAGCTGCTTACCGAAGACTTCGTTGAATTTTGGAGCTATCGGCAAAAGCTGGACGAAAGCGGAGGTGATCGTGGGACTAA AATCCCAGACTTGGATCAAAAGGACAATCGAGGATTTCAAACTGCGTGTGCTTGCAGATGGTGTCGCGTTAGCAACGTAC CGATGCCGTCATCAAAATGCTAATGGCGATGAGTCGTTATCAATGCGTAGCTCTGTTTGGAAAACCTACGAAGATGGTTG GCACATGGTGTTTCACCAAGGCACGAGGGTCTCCGAGTAG

Protein sequence: (SEQ ID NO: 159)

MDIRLEILALEQLLLEPESRKNDRLLKQLLTEDFVEFGAIGKSWTKAEVIVGLKSQTWIKRTIEDFKLRVLADGVALATY RCRHQNANGDESLSMRSSVWKTYEDGWHMVFHQGTRVSE.

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FIGURE 30C

RL059

DNA sequence: (SEQ ID NO: 38)

ATGACTTCCTCGCCCAACCTTGACCAGATGACCCCGGAACAGCTTCGTGCCTTGGCGGCACAGGCGTTGCAGTTGCAATC CCAGGTCGAGGCGATGAGCAGGAAAATCCGCAACAATGAAACCCTCATCGAACAGTTCAAGTTCGAAATCGCTCTCAC AACGCCACAAGTTTGCCAAGCGCAGCGAGCAAATCAGTTCGGCGCAAGGCAGCTTGCTGGATGACCTGCTCGACACCGAC CTTGAAGCTATCGAGGCCGAGCTGAAACAACTCCTTCCAGCTTCGCCACAAGCCGAGCCACGGCAATCCCCGAAACGTTC GCCATTGCCGCCGCAGTTCCCGCGCACGTGATTCGCCACGAACCTGAAAATACCCAATGCGCCTGCGGCTGCCAACTTC AACGCATCGGCGAAGACGTCAGCGAGAAGCTGGATTACACGCCGGGCGTGTTTACCGTCGAGCAACATGTGAGGGGCAAA TGGGCCTGCCGTCAGTGCGAAACCCTGATCCAGGCGCCGGTGCCAGCCCAGGTTATTGATAAAGGCATCCCGACCGCAGG GGCTGCCAATTGCCCGCTCGACCCTGGCGCAGTGGGTCGGACAAACTGGCGTGCGGCTTCAGCCACTGGTCGATGCACTG CGTGAAGCCGTGCTGAACCAGGACGTGATCCACGCCGATGAAACACCGGTGCAAATGCTTGCACCAGGCGAGAAGAAAAC $\tt GTGCCGGAGAACATGCACGCAACTTCCTAGGCGACTGGAATGGCAAGCTGGTCTGCGACGACTTCGCTGGATACAAGGCC$ GGTTTTGAACAAGGCATCACTGAAATCGGCTGCATGGCTCATGCTCGCCGCAAGTTCTTCGACCTGCATGTCGCTAACAA AAGCCAACTGGCCGAACAGGCGCTGCACTCAATTGGCGGTTTGTACGAGGTTGAACGCCAGGCTCGGGACATGAGCAACG AAGACCGTTGGCGAATACGTCAGGAAATGGCGGTACCGATCAGCAAAACACTGCATGACTGGATGTTGGCCCAGCGCGAC CTGGTGCCCAACGGCTEGGCCACAGCTAAAGCCCTCGACTACAGCCTGAAACGCTGGGGAGCGCTGACGCGCTACCTGGA -cgatggggctgtgeccatcgacaacaatcaggtggagaaccagatacggecgtgggcgctcgaacgctcgaactggttat TTGCCGGATCGCTGCGCAGTGGCAAACGAGCAGCTATCATGAGCCTGATCCAGTCCGCTCGCATGAACGGGCATGAT CCGTATGCCTACCTGAAGGACGTGCTAACTCGCCTGCCGACGTTACGGTCGAAAGACATCAGCCAGTTGCTGCCGCATCA GTGGGTACAGATCTAG

Protein sequence: (SEQ ID NO: 160)

MTSSPNLDQMTPEQLRALAAQALQLQSQVEAMSRKIRNNETLIEQFKFEIALLKRHKFAKRSEQISSAQGSLLDDLLDTD LEAIEAELKQLLPASPQAEPRQSPKRSPLPPQFPRTVIRHEPENTQCACGCQLQRIGEDVSEKLDYTPGVFTVEQHVRGK WACRQCETLIQAPVPAQVIDKGIPTACLLAHVMVAKFADHLPLYRQEKIFGRAGLPIARSTLAQWVGQTGVRLQPLVDAL REAVLNQDVIHADETPVQMLAPGEKKTHRVYVWAYSTTPFSALKAVVYDFSPSRAGEHARNFIGDWNGKLVCDDFAGYKA GFEQGITEIGCMAHARRKFFDLHVANKSQLAEQALHSIGGLYEVERQARDMSNEDRWRIRQEMAVPISKTLHDWMLAQRD LVPNGSATAKALDYSLKRWGALTRYLDDGAVPIDNNQVENQIRPWALGRSNWLFAGSLRSGKRAAAIMSLIQSARMNGHD PYAYLKDVLTRLPTLRSKDISQLLPHQWVQI.

RL060

DNA sequence: (SEQ ID NO: 39)

Protein sequence: (SEQ ID NO: 161)

 ${\tt MIRIDAIWLATEPMDMRAGTETALARVIAVFGAAKPHCAYLFANRRANRMKVLVHDGVGIWLAARRLNQGKFHWPGIRHGCEVELDSEQLQALVLGLPWQRVGTGGVISML.}$

RL061

DNA sequence: (SEQ ID NO: 40)

Protein sequence: (SEQ ID NO: 162)

 ${\tt MRQRSSYPKPFKAQVVQECLQPGATVSSVAISHGINANVIRKWLTLYRDQPVPASLPAFVPLKATPKRPAETSVLIELPM\ AGOMITVK.}$

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FIGURE 30D

RL062

DNA sequence: (SEQ ID NO: 41)

ATGGCTTTATCTCTTATTCGTAGTCTCACTGCGTCCGCCTCACGAAACATCTCGGCGTTGAAACGCGATGCCAAACGCTT GCAGAAGAACTCCTTTCTTGTGTTTGGAACAGAATATCCACTCAAGGTTTGCCAAAATGCGGTAGCAGTTTCTCGCGGGCT TCCGCTCACTCGCTGATGTCGATAAACTGGAGCAGCACATTGGCATGAATAGAAGCGCTCCATTCTGGGTGATCCGTGGC CGCAACGATACACCAGGGGGTACTGGAAGCGCTATATTGTTTAGACCTTGAATATACCGAGAATGGCCCCGTCGTTTT TACTGGAAACCCAAAGCACTCTATACTTCCAGCCTTAGTCCTTTTTCTTGAGCAAATGAGCTTTAAGAAACTACCCGGAC TAATCCTCATCGAAACAAAAGAGACCTCAATCCAAACAACCCATATATTCGACGCAATAGAAAAATTAGAAGTCGAAGAA ACTCTAAATAAATTTCGATTTCTTGACTTGCGAGACCGAAACCTTCCCGTTTCGCTTAGTACCGAGGCTCGTTGCTGGAT CGAGTCAATTGTCAGTTTATTGCCAAACGACATCCAAGAGGAAATACGTAATAAAGGATGGTCAACTCACTTAGAGATCA GTGCATATGAGCATGCAAAGTCTCGTAATCAAGTATTTGGCTCCTCCAACTTCCCTTGCGTCCCCTTCCTCCATAAAG TGATATACGCCGACCTCCTCTGGAAAAAAGCTCAGAGGAAACCTTACTTTATCTCATAAAAAAATTAGAGAATCGACAGT ${\tt TCCACACAGGCATTTCATGTGAGCATGAGAGTCGATGGCGGCCGTATGTCGTACTCTTCTCCAGGAATGATCCGGCTAGC}$ AGATGGAGCAGTTCCCTATGCTCCCAAGCTTCTAGGTTTAGGCGGCCATACGGTCATTGCAAATGGAATCACTGAAATTC $\tt CCGACGGGGATCTTTGGGGAGTTCTATGGCTACAAGAACTCACTTAAAGTCAGCTCCTTATCTAACGGAATACAGTTC$ ATGGGTAAGCATGTATCACTAAAGTAA

Protein sequence: (SEQ ID NO: 163)

MALSLIRSLTASASRNISALKRDAKRLQKNSFLVFGTEYPLKVCQNAVAVSRGFRSLADVDKLEQHIGMNRSAPFWVIRG RNDTHQGVLEALYCLDLEYTENGPVVFTGNPKHSILPALVLFLEQMSFKKLPGLILIETKETSIQTTHIFDAIEKLEVEE TLNKFRFLDLRDRNLPVSLSTEARCWIESIVSLLPNDIQEEIRNKGWSTHLEISAYEHAKSRNQVFGSSNFPCVPFLSIK SAIYQLISGAYPPLWMQPSSSGEISKVDIRRPPLEKSSEETLLYLIKKLENRQFHTGISCEHESRWRPYVVLFSRNDPAS EVLAGVIHSYFSWKQDRDHRSPTLYVSDGAVPYAPKLLGLGGHTVIANGITEIPDGDGLGEFYGYKNSLKVSSLSNGIQF MGKHVSLK.

RL063

DNA sequence: (SEQ ID NO: 42)

ATGAACGCTCTGACCCAACCGGCCGCCCTCGCCGCCTCCCACCTGAACATCAACCTGACCGACTTCATCGACGAGTTCGG CGACGAGCTCCTGGAGTCGCTCAATCGCTCCAACCCCCGGTCTATACCGGCTCCGTCAACGCTCACCGCCAGTTGGTGA TGGACCGACTCAAGCGCAAGCCCTTCGCGGCCCAGGCCGAGGTCGTCCAGGCCATCACCGCCCTGCTGCACCGTAAC GAGCAGGCCGGAATCATCAACGCCGAGATGGGCACCGGGAAAACCATGATGGCCATCGCTGTCGCAGCGGTCATGCACGC TACGACGGGCGCAGGAGTTCTTCATCCTCGGCCGCGTGCGGATGCGGATGGGTTTCCACTGGCGGCTCGCCTGCTGGAA GAAACGCGCCGCCGGCGACTGCTCGCTGCTGCCCGGATTGCGGACAGGTCCTCGAGGACCTGGAAGGCAACCTGG GGACGAGGGACATGAGTACAAGAACAGCGGCTCGGCCCAGGGCCAGGCCATGGGCGTTCTCGCAGCCAAGGCACGGAAAA CCGTGCTGACCGGAACGCTCATGGGCGGCTACGCCGACGATCTGTTCTATCTCCTGTTCCGCATCCTCACCCAGCGC ${\tt ATGATCGAGGACGGCTATCGGCCCAACGCGCGCGCGCAGCATCGCTCCCGCAGCCATGTCGTTCATGCGCGACCACGGTGT}$ GCTCAAGGATATCTACACCGAGCGCGACGGTGATTCGCACAAGACAGCGCGGGGCAAGAAGCTCTCGGTACGCACGGTGA ${\tt AGGCTCCGGCTTCGGCCCAAAGGGCATCCACCGCTTCGTATTGCCGTTCACCGTGTTCCTGAAGCTCAAGGATATTGGT}$ ${\tt GGCAACGTACTGCCCGACTACCAGGAGGAGTTCATCGACGTGCCCATGGCGCCTGAGCAGGCTTCGGCCTATCAGCGCCCT}$ GGCGGCCACGCTGACAGCGGAGCTCCGCCAGGCTCTGGCGCGACGAGATACCACGCTCCTGGGCGTGGTCCTCAACGTGC TGCTGGCTTGGCCGGACTGCTTTTCCGACCGGAGATCGTCAAGCATCCGCGAACCCGGGACACACTGGCCTTCGTGCCA GCGATCTTCGGTGACGAGCAGTTGATACCCAAGGAGCAGGTGCTGGTGGACCTCTGCTTCGAGGAGAAAGCGAAGGGCCG CAAGGTTCTGGCATACACCGTCTACAGCGGGACGCGCGACACCACGTCCAGGCTGAAGAAAGTGCTCGAGCAATCCGGGC TGAAGGTGCCACTACGTGCTTCGGTCGATACCGCTCGACGCGAGGATTGGATCCTCGACCAGGTCGATCGCGGCATC GATGTGCTGATCACCAACCCGGAGCTGGAGACCGGGCTGGACTTGCTCGACTTCCCGACCATCGCGTTCCTGCAAAC GGGCTACAACGTGTACACCCTGCAGCAGGCCGCGGCGGTCGTGGCGGATCGGGCAGAAGCACCCGGTGAGGGTGGTGT TCTTCGGCTACGCCGGCAGCTCGCAGATCACCTGCTTACAGCTGATGGCCAAGAAGATCGCTGTGGCTCAGAGCACGTCG GGAGACGTTCCCGAGTCAGGTCTCGACTCGTTGAACCAGGATGGGGATTCTGTGGAGATGGCGTTGGCACGACAACTCAT CGCAGCATGA

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FIGURE 30E

Protein sequence: (SEQ ID NO: 164)

MNALTQPAALAASHLNINLTDFIDEFGDELLESLNRSNPPVYTGSVNAHRQLVMDRLKRKPFAAQAEVVQAITALLLDRN EQAGIINAEMGTGKTMMAIAVAAVMHAAGYRRTLVVSPPHLVYKWRREILETIPAARVWVLNGPDTLLKLLKLRDQMGDA YDGRQEFFILGRVRMRMGFHWRLACWKKRAAGGQLLAACPDCGQVLEDLEGNLVTVEEFERGDRRTCSSCRGALWTLIR PGKPDGGNRRATILKSMCRIPTIGPVRAERLLNDFGEDFLATMLVDNVSEFINLMDAKGNFVFSDRQAKRMERSMANIEF GFGEGGYQPTEFIKRYLPPGYFDLLVLDEGHEYKNSGSAQQAMGVLAAKARKTVLLTGTLMGGYADDLFYLLFRILTQR MIEDGYRPNARGSMAPAAMSFMRDHGVLKDIYTERDGDSHKTARGKKLSVRTVKAPGFGPKGIHRFVLPFTVFLKLKDIG GNVLPDYQEEFIDVPMAPEQASAYQRLAATLTAELRQALARRDTTLLGVVLNVLLAWPDCCFRPEIVKHPRTRDTLAFVP AIFGDEQLIPKEQVLVDLCFEEKAKGRKVLAYTVYSGTRDTTSRLKKVLEQSGLKVAVLRASVDTARREDWILDQVDRGIDVLTNPELVKTGLDLLDFPTIAFLQTGYNVYTLQQAARRSWRIGQKHPVRVVFFGYAGSSQITCLQLMAKKIAVAQSTSGDVPESGLDSLNQDGDSVEMALARQLIAA

RL064

DNA sequence: (SEQ ID NO: 43)

ATGGCCCTCATGTTCCCGCGCTTGGCGCGCAACTTTGCACGCAACGGCTACTTCCCTACCGATGAGGTC GCGTCTGGAGAAAGCGTTCTACCAGCGCTGCCTGCCGTTGCTGCAGTACGGCGGCGTCATGGTTCTGATTGTTCCTCACT A CGTCTTGGACGATGAGCTGGCTGGTTGAGCAACCACTTCACCGGCCTGCGCATCTACGCAGCCGCGGATCCTACC $\tt CGGCCACCAGCGAGCAGCACCTCTACCGAGTAACCCTGGAGCCGGAGCAGTTCGCCGGTGAAATCCAGCGGCTGCGA$ GGTCTCTGGCCTGACTTCAACCTGCACTTCGCGCAAGCGGGGCTGCAGCCGCCCCACCAGTCCGCGAGCTGTCTCGCTG ${\tt GCACCTGGCCCTGGCCGCGGCGCGGATATCTGGCGTCGTGCGATCGGAGGCCGGATCCTGGTCGTGAAGG}$ GTGACACCTACAAGGACAAGGTCCGCAAGACCGAATTCACCGAGGACGACGACGGCAACATCACCGAGGTGAGGATCCTC ACCGACCGTTTCATCCCGATCATCCGGGCATGGGAAATGACACCCTCCTCGGTCAATCAGGGCCGCGTGCTGACCATCAG $\tt CTGGCCGGGTCGTAATGACCGCAGCCGTGAGCCACCTGGTGGAAACCGGTCAACTCAACCCAGCGCCTTTGCTGAAACGC$ $\tt CATCTGGCGGGAGATTGGGGAACGCCAGGAAGACTGGAACACCAGAGAGCCCTGAAGTTCGGCGATCGGCT$ GCTGTCGTCCTACGACATCGACGCCGGCGACGAATCCAGGCTCTGGATCATCACTGAGGCAGACCGCAGCTCAACCACGC TTTTGCTCCCTAGCGATTACTGA

Protein sequence: (SEQ ID NO: 165)

MALMFPRLARNFARNGYFPTDEVTLERALQALTLAPSGRMRICDPCAGEGVALAEAAHTLGRDQVQALAVEYDRERADHA RGLLDRVLHSDLFDTMISRQSFGLLWLNPPYGDLVADHSGASQYQGSGRRRLEKAFYQRCLPLLQYGGVMVLIVPHYVLD DELTGWLSNHFTGLRIYAAADPTFKQVVIFGIRVRRQDLARADANQVRSRLQAIGAGQEKAEEIPAAWPWEPYVVLPATS ELEHFYRVTLEPEQFAGEIQRLGGLWPDFNLHFAQAGLQPRPPVRELSRWHLALALAAGAISGVVRSKSGRILVVKGDTY KDKVRKTEFTEDDDGNITEVRILTDRFIPIIRAWEMTPSSVNQGRVLTISSSAATTEEAEEPQPEPAPAPALLISPGRV VMTAAVSHLVETGQLNPAPLLKRHLAGDWGTLDQEDWNTNQRALKFGDRLLSSYDIDAGDESRLWIITEADRSSTTLLLP SDY.

RL065

DNA sequence: (SEQ ID NO: 44)

Protein sequence: (SEQ ID NO: 166)

MPSPTPLYQIECPDLYVDACVCDEQCNLVFLSAWGRDTVTQEFLARLTLGREENGIDHFHIIVDGRRLPVFPNQDLLEK RTTRQFRGTLFGSLLNLWLFDRRASAPDRGNHLAFALLQRDEDPHQRLWPLVMETCPLPLLQHWREPVMEVLTQHQMLTA LPGTIGNVCAWRLALRVDVLEPTLGEVIRESILTTDAQAQA

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FIGURE 30F

RL066

DNA sequence: (SEQ ID NO: 45)

ATGATCCATTGTTCACCAACCTCACCCAGGAAACCCTCGCCTACCTCGAGGACCAACTGTCCAACAACGACGTCGCCGGCGACGACGACGACCTCATCGACTTGTTCATCGAGGAGCTGTCGCTGACCTTGGAGCAGGCGGAAGCGGCTGTCGCGCTACGCGATCAGTACCTCTGCCAGGTCTTCCTGATCGGCCAAGGGCCGCTGCACCAAGCCGATGGACTCAGCTTCGACCCTCACACCCAAGAGCGTTCGGTAG

Protein sequence: (SEQ ID NO: 167)

 $\verb|MNPLFTNLTQETLAYLEDQLSNNDVAGDDELIDLFIEELSLTLEQAEAAVALRDQYLCQVFLIGQGPLHQADGLSFDPHT | VSUP |$

RL067

DNA sequence: (SEQ ID NO: 46)

Protein sequence: (SEQ ID NO: 168)

MGWLFSHQTKEDLLRELLAPTSTFAGSTEVLAHAVSGNELWTVVKRTFHLAGFYFGKPAGHSITMIELHLLDCSAGQWGY KTIPESAGPFYYGCPLEFLDLAHDEINQEWRKRLTHEHQA

RL068

DNA sequence: (SEQ ID NO: 47)

ATGAAATCGATCTACAACACCCCAGGCTTCAGCGAGGAGTTGTTGCTGGTTTGCGCCTCGCTGCGCGAGGTCGGACTGGA CAATCTGGCTGACCAGTTCCGCCGGCAGTGTTCGACCGATCCGTCGTCGACCAGGCCATCATCGCACTGCGTGAGCGGG TGAAGACCCCTTCGCCGGAGCATGCGGCCGACAACGAGCCCTGGTTGTACTGCGACTGGCAGGCCAGGCAAACAGCTTAC CGGCTCCTCCAGCGCCTTGAGCGCGCAACACGCTGA

Protein sequence: (SEQ ID NO: 169)

MKSIYNTPGFSEELLLVCASLREVGLDNLADQFRAAVFDRSVVDQAIIALRERVKTPSPEHAADNEPWLYCDWQARQTAY RLLQRLERATR

RL069

DNA sequence: (SEQ ID NO: 48)

ATCCCTCACCACGATCCCGCTTCGGCGGGATCATCCTTTTCGCAGGTCATACCATGATCACAGTTCCCGGACAGTTGGC
CATTCGAACCATCAACGGTCGCTATGGCGAGTTCAATGTGGGAAAACTCTGGACTTCGATCGGGGAGTTCATCATCAAGG
ATGCCTTCCTGGATCAACACCCGAAGGCAAGTACCGCGGTGATTTCGTCATCGCCAATATCCGCCCCCCACCACTACTCC
GCCGGCGGTCGGCTAGTCATCGAGATCCGCGCCATAGTGGACAGCATGACGCTGAACGATATGGACAGCCTCAGCGACGA
GGAGGTAGAGCGTCTTTCCGGCAATGAGGTGGATCCGCCCACAATGAGTCCCGC
CGATACCACCAAAGTCGCCGTCACCCCAGAAGTCGAAGCCTCTCTGGCCTCCTCGCTGCACCAGCACCCCCACATCTTCGGTATG
GACACTCCGGCTCCTGCAGAGCAGGCCGCCTCTCTGGACACAGACCGGATGCAGAACTGTTCGGGACGTCTTGGCCGCT
AGGCGAAATCGTCAAGCTGGACACCACGGTCGACCGCAAGCGCCCCTTACGCCCACAGTGCCGCTCTGGCCGCT
ATGAGCTCGACTTCAAACAACAGGTGGGACCCCCCAAGGAGGCCCCCATGA

Protein sequence: (SEQ ID NO: 170)

IPSPRSRFGGIILFAGHTMITVPGQLAIRTINGRYGEFNVGKLWTSIGEFIIKDAFLDQHTEGKYRGDFVIANIRPHHYS AGGRLVIEIRAIVDSMTLNDMDSLSDEEVERLSGNEVDPLDEVPEIOLPTVVPAIP

RL070

DNA sequence: (SEQ ID NO: 49)

ATGACCTCTCTCAACAACCACTCCAGCGCAGGTCACACTGCTGCGTACCTCAAACTCCCGATCGTTCTCACCAACGCGGC CTGGCTGCGCCTGGTCTATCTCGCCAACCCTGCCAGGGTCGACGAGATGGGCACCCGGCTGGCCAGTGTCGTTCAAACCG CCTGGCAGGAGCTTTCTCTCCAGCCGACCGCGAAGCACATCCAATTCCACCTGTACCACAAGGAGGAAGAGGGGCAGGAC CGCGCGCTCGCGCTGCTGGTTCTCTCGATAGTCGAGCCGTCCGATGAGCCTTCCTACCTGCGCATCGAGTTGCAGGAAGA GTGCCTCGCCGAACACCCGGTTACCGAGTAG

Protein sequence: (SEQ ID NO:171)

 ${\tt MTSLNNHSSAGHTAAYLKLPIVLTNAAWLRLVYLANPARVDEMGTRLASVVQTAWQELSLQPTAKHIQFHLYHKEEEGQD} \\ {\tt RALALLVLSIVEPSDEPSYLRIELQEECLAEHPVTE}\,.$

PKSPSPQKSKPLCLAATRDAPFGM

 ${\tt DTPAPAEQAASLDTDADAELFGTVWPLGEIVKLDTTVDRKRLRQQCVRLGALGYELDFKQQVWTRKEAA}$

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FIGURE 30G

DNA sequence: (SEQ ID NO: 50)

ATGACTCAACTCAACCCGTTTATTCGCGGCTATGAGAGTTTCCGCATCGAGCGAAACCTGCAGATCACTGACGAAGGCAA CAATCTACCGTGCTACCGCGCTCTGCATGAAACCCAGCAGCACCTCCCAGACGAATATTTTCAGTGCGAGCTGTGCTACT TCAATAACGATTTCGCCGTGGTAGTCCAAGAGTTAGACGATGAAAAGGGTTGAAAAATGCCCTCACCAAGGAATAGTGAGA AACGTACTTTACAGCATCTACGGTGAGCAGGACGGCAGAAAAAAGCTTATCGGAGATCAATACTCACTGACCGAAGCCGA GAGTGTCGTTCGATACCTTTCGTTCGGCGGCGGTTATAACCCCTGCTGGGAGATCAGAAAAACACATCTACCCATCAGCG CGTGGAATAGCCTCTACGAAAGGTTCTCGACCAAGATGCCAATCCGCTTGCCCTCGGTGTTGGTATCGCTCTTCTGGTGT AACGAGCACGGTGCCGTGGGCTTTCGCTTGCACAACACCCCTTGGACGGTGAGTGTCTGGAGATCCTGGAGATGACCGC AGCCGCTCTTCGACAAGAACAGCTTGCCTTCGGCCTCGACGAACACCTTGTCGATCTGCTTCACCTCGCGGGACAAGCAG ACATTCGGCTCCTGGTACTTGATCCATTCGCGCCCACGCTCAAGGGCCTGCCGCTTTATGACGATTGA

Protein sequence (SEQ ID NO: 172)

MTQLNPF1RGYESFR1ERNLQ1TDEGNNLPCYRALHETQQHLPDEYFQCELCYFNNDFAVVVQELDDERVEKCPHQG1VR NVLYSIYGEODGRKKLIGDQYSLTEAESVVRYLSFGGGYNPCWEIRKTHLPISAWNSLYERFSTKMPIRLPSVLVSLFWC $\tt NEHGAVGFRLHNTPWTDECLEILEMTAAALRQEQLAFGLDEHLVDLLHLAGQADIRLLVLDPFAPTLKGLPLYDD.\\$ REGREE RESIDENCE DEL DESTIMANTA DE CONTRACTOR DE LA CONTR

DNA sequence: (SEQ ID NO: 51)

ATGGGACTGGTGTTTCCTACCGAAAGGAGAATCACCATGCAATACGGAAAGCTGGCGCTCGCCCATCTCAGCCTGGAACT GCCGTTGCAGGTACTTATGAATAAGAACCGTGCTTACTACATCGGCACTTCTGACGAAGAAGGACCAGCCTCGCGCGAGT CGGTTGAATATTACCCCTCACGCGAACTTGCCCAACAGGCATTAGACCACGGCACTTGGACGCAACTGGAATATTAA

Protein sequence: (SEQ ID NO: 173)

 ${\tt MGLVFPTERRITMQYGKLALAHLSLELPLQVLMNKNRAYYIGTSDEEGPASRESVEYYPSRELAQQALDHGTWTQL{\tt EY}.}$

RL073

DNA sequence: (SEQ ID NO: 52)

ATGGGAAATGTTTGGCGATTATGCCAGGCAGATACCTGGGCATTGTTGTTGGCCAGGAACAGCCAGGCGAAGTTGCAGA ATTTGGATGTTGCTCATGATGTCCCAGATAATGGAGAACACCACGCCCTGGGGGGAGATGGTGCCCCCCGGATGGGTA TGCGATGAAGAGTGGCGCATAGCGTAG

Protein sequence: (SEQ ID NO: 174)

MGNVWRLCQGRYLGIVVGQEQPGEVAELTAEQQLVLDVAEANLLNFRQGGQFYDLDVAHDDLQIMENTTPWGEMVPPGWV CDEEWRIA.

RL074

DNA sequence: (SEQ ID NO: 53)

CAAGTATTTCGACCTGCACACCGCGTATCGGCTACCTCAATCGCATCCGCGAGGTACCGATCCGCCGAGGTGAACCAT ${\tt CGATATCTGGGCGGATCCCTTCATCCACCAGAAAGGCGAGAAACAAGGCAAGCCCGACGCAAGCCTCAAAGGCCGGCTGC}$ GGCGAACCTCAAGGTGAGCCCGCAGCCCCGCTGAGCACGCTGAACAAGCCGCTGCTTGA

Protein sequence: (SEQ ID NO: 175)

LTGKVFLRFRLRNWRIIMSNNTQAQEAKYFDLHTTGIGYLNRIREVPIRRGEPFLAVTVAALHGAADSVEYSYIDCKVVG AQAEKLVRRCKEAVEAKKKVLISFRIGDIWADPFIHQKGEKQGKPDASLKGRLLFISWIKVDGTTVYDAKEEAEKAQQGK GEPOGEPAAPAEHAEQAAA.

RL075

DNA sequence: (SEQ ID NO: 54)

ATGTCCAAGCAATCCACCAGCTTCGAAATCGGCTTTGCCCTCGGCAGTGTTGTGCGTGAGTTCCGCAGAGCGCTCAGTCG CCGCTGGCGAGCTAGAACACATCAGCGACATCCCAGCCATCGTCCGGCTGAAGAAGGTCAACCTGAATGACTGGTATCTA GCCAATACGCGCGAGGTGCAAAAGCCCAAGCGCGCACGCCAAGCCCAAGCCGACGCCAAAGCTGAAACGCC AGTCAGGAAGGAGCTCAAGATGGGTTCCCTCGACCATTTGATTGCACCCAACTCCGAAAGCGAAATGGGGAGGCCCCCTC TCCAGTTAGAGTCCCTGAACGATCATGAGATTGCTCTTTTGCCAGCACCTCCTGGTAGCGCAGTCTCTTGGGAACTCCAT CGGCGTACTCAGGAGCAATACCAACAACGCTGGCAGGACTACTTGTCCACCATGACGGATGAACAAGTAGCTGCTCTCGG CCGCTAA

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FIGURE 30H

Protein sequence: (SEQ ID NO: 176)

 ${\tt MSKQSTSFEIGFALGSVVREFRRALSRPPVVVQAQAPVALRVQRIDPAFLAGPTAGELEHISDIPAIVRLKKVNLNDWYLANTREVQKPKRARKPKPAKATAKAETPVRKELKMGSLDHLIAPNSESEMGRPPLQLESLNDHEIALLPAPPGSAVSWELHRRTQEQYQQRWQDYLSTMTDEQVAALGR.$

RL076

DNA sequence: (SEQ ID NO: 55)

ATGGTGTTTCTCCTGCAGGTTGAGGGTGCGAGAAAACACTGGCCCTGGCGGGGAAGTGGATTCCCCGCTGGGTTGCGGA
AGGGAGCTTCTATCGACCGAGGCCGACCGACCGCGCTACCAGAAGCTATGCGGTCTTGGGTTGGATCAACACGGTGGGCT
GTGCTGCAGCATTTCGGATCCGAGCTGCATGGGGGCATGTCGCTGACAACGTCAGCAGATCACGCGTTCATCATCGAAGC
GGGGGCGAAAGTGTCAAGGTCAAGCAGGAGGGGGGAGCGGATGCACCGGGCGGAGAGCGAGGGCGGAAGAGCCCGGCTGG
TAGAAACCCTGTCAAAGGTTTCCCCAGCCGTGTCTGGAAGGGGAGTCAAGTGAGCCACCTGTGGTTGAATCGTCGATCCC
TGGGCATTGATCGTCTCGATCCCATCACCCGGCCATTATCGTGGCTTGCCAGCAACAGTAGGCACCGCATCCGCGTACA
AAGGGAGCCCTGCGTATCACCCGGCGGCCACCGGCAGGAAGAGGATCCCGATGGGTAGCCTGATAGTCCTGGAGCAGGA
GCATCAGGCTACCCATGGAGAGGGGGAAAAGGAGGGGCCGTAACACCAGTACGACCCTTAAATCGAGGAAACACCGAACCT

Protein sequence: (SEQ ID NO: 177)

...MVFLLQVEGAEKTLALAGKWIPRWVAEGSFYRPRPTDRATRSYAVLGWINTVGCAAAFRIRAAWGHVADNVSRSRVHHRS —GGRKCQGQAGGGADAAGGERGRKSAAGRNPVKGFPSRVWKGSQVSHLWLNRRSLGIDRLDPITRPLSWLGQQTVGTHPRT KGALRITGGPPAGRRIPMGSLIVLEQEHQATHGEGKRRGRNTSTTLKSRKHRTS.

RL077

DNA sequence: (SEQ ID NO: 56)

Protein sequence: (SEQ ID NO: 178)

MPLMWIVLVLALITGTWLSVQSDHATSSAELAEVDTLARSLLLFRSSLAEYAHANPGFTGSPADSALGLPAWFRKPARLQ GYIAAGTSYAFIASPPAGLAAAVDAGTESDLVGVRRNGQLVTRRLGATVIALPTPIPEGAVVAVK.

RL078

DNA sequence: (SEQ ID NO: 57)

ATGAGGAGTACGCGCAGCAGTGGATTCATCTCGATCGAACTGATGATCGCCCTCGTCGTGATCGCCATCGCGACCGCCGG CAGCGGAGAAGTACCTGAAGGACAACTTCAGCACGGTTCTGGCCAGCGCCCAGGGCCCCGGCGGTGATCACCGTC $\tt CCGCAAGCCGGCGCCAACCAGCTCGAAACGCTGATCGTGACCACGGGTGGACAGGTAGCTTCCGAACTCTCGATCCGCC$ GGATCGCGCAGCTCATGGGAGCCACCGGGGGCTACATCTCGAAAACCAACACCAGTATCGCCCAGGGCGCCGCCTGGCAG GTGGCCTTAAGCAATTTCGGTAGCGCTCCCGGCGCTGGACATCTGGCGACGGCGCTGTTCTTCCAGGACGGCGCCATCGC CAACGAGTACCTCTACCGCAATGCCGTCCCGGGTCATCCTGAACTCAACCGGATGAATACCACGCTGGACATGGGAGGCA ACAATATCGCCGCAGCCGGGCCATCACGGCCAGCGGCAACATCACCACCAGCGGGACATCAGCGCGCAACGTGACA GCCACTGGTACGGTGAAAGCCGGCACTGCTGACGTCGCCGGCGAGACGTACACCGGAGGCTGGTTCAGGACCCGTGGTGA CACGGGCTGGTACAACGAGAAATGGGGCGGCGGCTGGTACATGAGCGACAGCACCTGGGTGCGCTCCTGGATGAACAAGA TGCATGGTCAGGATAGCGCCATGGTGAACTACGACTACGTCCGCTACGCGATCACCTGCGGCGGCCGATTCTGCGCAGTG CTACAAGACCCCCGACTCGACCAACGTGACCGTTACCTGCGTGAACTAG

Protein sequence: (SEQ ID NO: 179)

MRSTRSSGFISIELMIALVVIAIATAGGISVLMSYLDGLDEQHAAQQQQQVAKAAEKYLKDNFSTVLASAGATAPAVITV PMLRNTRYLPAGFRDTNIYGQQYQVLARKPAANQLETLIVTTGGQVASELSIRRIAQLMGATGGYISKTNTSIAQGAAWQ VALSNFGSAPGAGHLATALFFQDGAIANEYLYRNAVPGHPELNRNNTTLDMGGNNIAAAGAITASGNITTSADISARNVT ATGTVKAGTADVAGETYTGGWFRTGDTGWYNEKWGGGWYMSDSTWVRSWMKNVYTGGEMKAGKLTAEGRTEVGEYLQL KGVATEGANCSPNGLAGITSTGLWLSCQNGKWGRTAASMRLNTTAGVIKDWCTLHGQDSAMVNYDYVRYAITCGGRFCAV GFNOTFGTNYSFGLITEIGPGFNYPEPYKTPDSTNVTVTCVN.

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FIGURE 301

RL079

DNA sequence: (SEQ ID NO: 58)

Protein sequence: (SEQ ID NO: 180)

VSVNPIIQAQFVDLYLGEGFADVKGLAGAGARRVEVPREWESHVQELLQICRQTLEELQDPEFAIVVDGVLLRVTLLEDA FSGSVFVLRRSSAQLREFQEIGYPSEVVSALMDPQLQGLVLFCGEMATGKTSSAASLLLARLQELGGVGCAVEDPQETNL SGQHGLGRCIQVRTSRRSGGYSEALLRTLRAGADLVLIGEIRDEDTAYQACKASLTGSLVIATIHAKSCHQAIERLVTLA QPLARNAYDVVAEGIQAVICQALESDGSSRRLTAEPLLFTGDDGPSMRDKIRRKEAHLLQDDQARQSRQSLWR.

RL080

DNA sequence: (SEQ ID NO: 59)

Protein sequence: (SEQ ID NO: 181)

MSTTQRTSRPTQGGFVSIEMIIVLIIIAIGVGLGLAAAAGMFSSSNANEEQRNISVIAANARALKTSSGYGSSGTNLIPS LIAINGVPKNMSVSSGVVYNVYGGSVTVSSTGMGFSITTSKLPQDACITLATKIAKNTFEQTKINSGSSITGEVTTAAAT QACSSDSNSITWTYSS

RL081

DNA sequence: (SEQ ID NO: 60)

Protein sequence: (SEQ ID NO: 182)

MGGFWEQLQFAFYSKQFGRKERLQFYESMSTLLENGVPLKDAVAEVHKIFAHEGQHPFHPVAIASREALMGLSNGKRLAT
AMALYLPAQERALIEAGEMSGNLVQAMGDAVSLVEAQARIRATIWQALLYPSALSAMMVFLLCIVAYRMVPSLARLSDPV
TWTGPLATLNAIASFVTGPGIYVLVAVITLTVVVIVTLPTYRWKGRVWLDRTLPPWSIYRMLQGTTFLLNMAVMLNAGIR
PYDSLASMIKISPPWLKQRLEAARYGVGLGQNLGVALRSAGHDFPDRQAIQYLCÏLANRGGFSEALVKFSRRWQETSLKQ
_IELAAGLVKNFALIFIGALMILVLLGAYQAQQLIQSMNH:

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FIGURE 30J

RL082

DNA sequence: (SEQ ID NO: 61)

 ${\tt TACACGTTCTGTCGTTCATCGACCGTCTCGATCGCCGTGGCTTCCGATACCAGCTCAACCTCACCGACCTGCAGACCATT}$ GGTCAAGATCATTCGTAAGGCCACTGAGCTGCGCGCCAGTGACGTGCATTTCGTCGTGAGTCCCGCCGGCACCGGCAGCA $\tt ATCTACCAATCCATGTGCGACGTGGCCGAGCCACTGTTCAAGCCGCAACTGGACCAGGACGCGCGGATGAGCCAGACCTT$ CCTCGACAAGCTCCATGGCGGATCCAAGCACATCCTGACCATCGAGGATCCGCCGGAATACCGCATTCGCGGCGAAGGCA TCAACCAGACCCCACTGGTCTACGACGCCACCGACCCAGACGCAGAACGCCAGGCCTGGGCCGGGGCATCGCCAACGGC ATGCGCCTGGATCCGGACTACATGATGATCGCGAAGTACGCGACCTCTTCGCCGCTGTCGCCGCGTTCCGTGGTGCGAT GACCGGGCACGGCCTATGGTCGACCCTGCACACCAACAGCGCGATCGGCATTGTCCAGCGCCTGAAGGACCTGGGCGTCG ${\tt ACCCCGGCTTGCTGATCCGGCCCTGATCAACCAGAGCCTGCTGCCCAAGCTCTGCCCCACTGC}$ *AAAGTGCGCTTCCAAGACGACCAAGACCAACTCGCGCCCGACTTGGTCGAACGGGTCCGACGCTTGACCGATGTTTCCCA -GGTTCACGTCAAGGGGCCTGGCTGCCGGGCGTGCCTGGCTCCGGGGTCAACGGCCGCTCGATCGTCGCCGAGGTGGTTC TGCCCACCCTCGCCTTCATGCGTGTGTTCGCCAAAGGCGGCCCAGCCGAGGCACCAACTACTGGGTCAAGACCATGCAG GGCATCACCAAGCACGCCCACGCCATCCGCCGCATCAACGAGGGCATGTTCGACCCGCAGATGGTCGAGGATTTCATTGG GCCACTCGACTTCGATGAGCATCTGCTCGACGACAGCTTCTACTCGCAGGAGGCGTGCTGA:

Protein sequence: (SEQ ID NO: 183)

MTNLQIAALAQPSMVTQLLTADGGEWEVSKHLQEIMALAADGTLYLSESHQNDIHVLSFIDRLDRRGFRYQLNLTDLQTIHQLYRAVAMDGLVDSDGQRATQMQERVVKIIRKATELRASDVHFVVSPAGTGSKIRFRVDGLLKTVEQFRSQELHELCATIYQSMCDVAEPLFKPQLDQDARMSQTFVEKLNLFSARIATRPRAGGFLMILRLLYDDTGLDSLEQLGYLPEQNALFDRMMRMPYGINILSGPTGSGKSMTLKVTLEGLDKLHGGSKHILTIEDPPEYRIRGEGINQTPLVYDATDPDAERQAWAAGIANGMRLDPDYMMIGEVRDLFAAVAAFRGAMTGHGLWSTLHTNSAIGIVQRLKDLGVDPGLLFDPALLTGLINQSLLPKLCPHCKVRFQDHQDQLAPDLVERVRRLTDVSQVHVKGPGCQACRGSGVNGRSIVAEVVLPTLAFMRVFAKGGPAEARNYWVKTMQGITKHAHAIRRINEGMFDPQMVEDFIGPLDFDEHLLDDSFYSOEAC.

RL083

DNA sequence: (SEQ ID NO: 62)

Protein sequence: (SEQ ID NO: 184)

 $\label{thm:matting} $$\operatorname{MRTEPIGMAVAVLFLLASGQACAGTVGELAEIQAQAILTEAKVRLATAQRQLEGKGETGQVVSAQGQTFAMPVPAAPPTI$$$\operatorname{TQPVPPVVRTIYGAGGKMTATFLFPGGYEVDAASGAELPGKYRVESISLDQVVLTDKDGNRVPVGFSSVAPTQASSTAQGASVPPALPGAVPQPFIQ.$$$

RL084

DNA sequence: (SEQ ID NO: 63)

ATGGAGAAGCCTGACCTCGGCAGCCGTGGACCAGACGTCTCGATCCTGAGCTACCACGGCAACAAGTTCGTCAGCGGCCT TTGCCATCCGCCATTCACCGACGGTGATCCAGGCCGGCTTCGTTTCGAAGTCGCAAGGCGCAGTCAAGGGGATGTACTCC $\tt CTGGCCTCGGCGCTTTCAGGCCAGTTCGACGGCGACTTCCTGGCCTGCTGGAAAGTCGACGAGGACCGCTACGCGCTGGT$ TCTCTACGCGCGGCGTGCTGCGAAACGCACAGGTCTTCGTTCCCGAAGGGTTCGATTTCCCCGTCAAGGACTTCGACATC GAGGAACTGCTCGCGCCGAAGCGCCTGCGGCGCGACTACCGCCTCCGGCAACTCACCTTCGGCTTGTCCGCCAGGGAGTG GACGGCAGTGGCCCTGCTCGGTTGCGTGGTTGGGTCGCTAACCGCCTACTACCTATGGAATGCCCACCAGGAAGAGC TCGCCAGGCAAGCCGCGCTCCTCGAGGAGCAGAGGCGCCTCGCCGAGCTGGCCGAGAAGAACGCCCAGGCCAAGCAGCCG ${\tt CTGGACCTGGCGTCATTGCAGAAGCCTTGGACGCTCATACCTGACCTCGAGGACATGCTACGCGCCTGTAGCAAGGCAAC}$ ${\tt GGGGGTACTGTCGATCCAGGGCTGGCTCTTCGAATCCAGCAAGTGCGACGGCAGGGTCCTGGTCGCCACCTACC}$ GACAACGGCAACACCGCGGCCCTGAAGGTCGATCTGAAGGTTGCCATCGGCAGTGATGAGCCGCTACTGCCGGCGGACGA $\tt CGTTCTGCAGGCGTGACGAGCCACCTGTACCGTCAAGGGGTCGAGCCCAAGCTGTCGATCAGCCAGGAGACAACTCCGC$ $\tt CCCTCCCTGGCGGGAAGCTGCGACTGAACAGCAAGTGGTGTTGCCTTCCTGGAAGAAATTCACCTTCAGCGCCCCAGACC$ CGGCTCCCGGCAGACCTGACCTTCCAGGGGCTGCCCGCTGCCGGTGTCCGCATCACCAACCTCGAAACCACGCTCAAGGA CAGCCAGTTGGACTGGACTGTCACAGGAGAAATCTATGCGAACTGA

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FIGURE 30K

Protein sequence: (SEQ ID NO: 185)

MEKPDLGSRGPDVSILSYHGNKFVSGLFWRPLSSQRQYMKEARKLGKEEHLDIVAIRHSPTVIQAGFVSKSQGAVKGMYS LASALSGQFDGDFLACWKVDEDRYALVATLDGAIVPGQDLVTTLDEARDRVRKLSTRGVLRNAQVFVPEGFDFPVKDFDI EELLAPKRLRRDYRLRQLTFGLSAREWTAVALLGCVVGGSLTAYYLWNAHQEELARQAALLEEQRRLAELAEKNAQAKQP LDLASLQKPWTLIPDLEDMLRACSKATGVLSLSIQGWLFESSKCDGRVLVATYHRTGNSTAADLTAASQHLFADRPAFVI DNGNTAALKVDLKVAIGSDEPLLPADDVLQALTSHLYRQGVEPKLSISQETTPPLPGAEAATEQQVVLPSWKKFTFSAQT RLPADLTFQGLPAAGVRITNLETTLKDSQLDWTVTGEIYAN.

RL085

DNA sequence: (SEQ ID NO: 64)

ATCGTGTGCGAAGCTACGGCAGATTCCGCGTCTACGATCGCAGCGCAGGTGCGCAACACCCGACCGGATCGGCGCGATAC GGTGGTGTTCTCCGACAAACCCTGGGTCAGCACGAAACCCCTAAGCGTTTCGCACACCTTGTCCAGTGACTGCATCGTGA ACGCCCGACGCGCTGAACCCGGCCGCCTTCGCCGTGCAACCTCAGCAGCGCGCGGCGAGCAACGCCCCGCCGCCCATCCAAGG CGGCCAGGACATGGCCACCATGCTGTTTCCTGCCTCGCCAACGGCATGTCGCTCGGTGCCGGCGGCAGCATGGGGT CGAGCTTCGGGTCCTACGGTCCGCGGTCTCTGTACAACATCAAATGGAACGGCAAAGTCAGCGGGTTCCTCGATCTCATC CCGCATGTACGCCTTCGACGACGTCAACACGGTGGACTCCACCGTGCGTTCCGGTATGACGACGGCCGCCGGCATCAGCG GAGCTGAAGACATCGATCCTCAGCGACATCGAGAACAGCATCAACTCGATGCTGACGCCGAGCATGGGGACGCATGTCGCT ACGAGAGCATCACCAAGCAGGTGCTGCTGAACGTCAACGTGCTCTCGGTCGCCCTGACCGACAAGGATCAACTGGGGATC GACTGGAACCTGGTCTACAAGTCGCTCAACAACAAGTGGGGCATCGGCCTGAAGAACACCCATGCCGGGCATCGATCAAAG CCCAGCAGGGCCGCTCTCGACCGTCCGATCCCGTCCGTGACCACCTCCAGTCGGCGCCGATCCAGATCGGC $\tt CGCTACGACAGCTACCTGGCCTCCAGCCAGATCTCCAACGTCGCCAGGTCGGCAGTACCACCTCGCTGATCCCGGGGCGCCCCAGGTCGCCAGGTCAGG$ TGACCTCCCGGCCGACGTTCGAAATGCAGACCAGCGGGGACTCCAAAGCCCAGTTCCCGAGCTACGACATACAACTGTTC GACCAGAAGGTACGTCTGCGCAGCGGCGAGACCTTGGTACTCTCCGGCTTCGACCAGACCACCGAGGACCACCAACAAGGT CGGCACCGCGACGCTGGGTTCTTCGGTCTTGGCGGCGGGCTGACCCGCAATACCAAGCGCGAGGTCATCGTGGTGCTGA TCACCCCGTCGTGCTGGGCTGA

Protein sequence: (SEQ ID NO: 186)

IVCEATADSASTIAAQVRNTRPDRRDTVVFSDKPWVSTKPLSVSHTLSSDCIVTWRPAGAASLQEAAQEVINQCHMAVSI
TPDALNPAAFAVQPQQRASNAPPPIQGGQDMATMLFPASVANGMSLGAGGSMGSSFGSYGPRSLYNIKWNGKVSGFLDLI
AARAGVSWRYNPTEKRVEFYYLDTRTFRMYAFDDVNTVDSTVRSGMTTAAGISGDGSGSTGQNGSSGISGDSGSKQTTSS
ELKTSILSDIENSINSMLTPSMGRMSLSRATGTLTVTDRPEVLNRVQQLVNRENESITKQVLLNVNVLSVALTDKDQLGI
DWNLVYKSLNNKWGIGLKNTMPGIDQSAISGSVSILDTANSAWAGSKAMVQALAQQGRVSTVRSPSVTTLNLQSAPIQIG
RYDSYLASSQISNVAQVGSTTSLIPGAVTSGYNMSLLPFVMESGEMLLKININMTSRPTFEMQTSGDSKAQFPSYDIQLF
DQKVRLRSGETLVLSGFDQTTEDTNKVGTGDAGFFGLGGGLTRNTKREVIVVLITPVVLG.

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FIGURE 30L

RL086

DNA sequence: (SEQ ID NO: 65)

ATGACCAGGCAGTTGACCACTCTCACGCTGTGCCTGCTCGCCAGCTGCACGACCCACAAGGCTGAGCCGGCCAGGCC AGCCTTCGACAGCAGCCGCAATCCAGACCTGCTTTCTCCGGACCTGTATCCAAACGGTGTGCAGCCGGAGAAAGAGCCCG TAGTGCGCTATGGGCGCTACACCCTGGTCAGCACCCAGCCTGATGCCGGTCAACGCGACCTGATGGCCCAGATCATCGAC GTAACCATCCCGTCGAGCATGAACCCGAGCGTCAAGGACGCCATGCAGTACGTGATGAGCCGCTCGGGTTACTCGCTGTG CCCGGCAGACGCCGGTCATGTGAACATCCTCTACACCCGGCCGCTGCCGGCAGCTCAGTACAAGCTCGGCCCGATGACCC TGCGCAACACCCTCCAGGTCCTCCCGGCCCAGCCTGGCAGGTTAAGGTCGACGAGGTCGCGCGGCAGGTCTGCTTCGTG CTGCGCCCGGGCTATCAACTTCCCCCGGCGCCGAGGCCGAAACCGGTCCAGCAACTGTATGCGAAGCCCGCTGCCCCAAC TCCGCCGGCGGTAGCGCAACCCTCCTCCACGGAGAAAGTCAGCACGCTGGAGTCGCCCATCGTGGTCGCCTCGGTGCCGA AAGGATGGCCACCCTCTTCTCCCCCGCGGCTTCGGCACCGACCAAGCCTGCGGCCTCCGCCGTGAAGTCCACGCCGCC GGTCAGCCGAGACGGGATCAACCCTGCGCGACACCTTGGAAGCTTGGGCAAAGCGCGCACGCTGGACCGTCCGCTGGGAG $\tt CCGCAGGATCTCAACTATCCGAGGGCTCCACTGACCTTCCACGGCTCCTTCGAGGACGCGGTATCCGAGCTGTTCCC$ ACTGA ${\tt CCTGTATGACGCTGCCGAACGGCCCTTCCTGGTGAACGCCAGCCCGCAGTCCCTGATCATCAACGAGGGCGCAAGA}$

Protein sequence: (SEO ID NO: 187)

MTRQLTTLTLCLLLASCTTHKAEPARPAFDSSRNPDLLSPDLYPNGVQPEKEPVVRYGRYTLVSTQPDAGQRDLMAQIID VTIPSSMNPSVKDAMQYVMSRSGYSLCPADAGHVNILYTRPLPAAQYKLGPMTLRNTLQVLSGPAWQVKVDEVARQVCFV LRPGYOLPPAPRPKPVQQLYAKPAAPTPPAVAQPSSTEKVSTLESPIVVASVPTPAPITTSHAPAKKPESTTVLPPAAPA ${\tt KDGHPSSPPAASAPTKPAASAVKSTPPTPPTVASAPPVKVLTPPEPSRPLAQAWSAETGSTLRDTLEAWAKRARWTVRWE}$ PQDLNYPIEAPLTFHGSFEDAVSELFPLYDAAERPFLVNASRPQSLIIIKERKN.

RL087

DNA sequence: (SEQ ID NO: 66)

TCCAAGCCTGGCATCAGTTAACCCCTTGGTAGTGGCTGGATTCAGTACTATCCTGTTTCCTTTCTCGGTAAGGCTTGTTG AAGACTTCGCTTTAAAATATACGGAAAAAGAGTTCTGGGTCACAGGTTTTTTCTCCGAAAACCCCTGCAAAAACAGGATTG ${\tt TATGCAGTCTTTTATTTGGTTATTTGTTTTCAATTCCCTTGGGGATGATTTTTTTATTCTATAAATACGGAAAGGC}$

Protein sequence: (SEQ ID NO:188)

LSFKYYWAKFFWGAFFFVLVAWKGSVFPSLASVNPLVVAGFSTILFPFSVRLVEDFALKYTEKEFWVTGFFSETPAKTGL YAVFYLACYLFSIPLGMIFLFYKYGKAS.

RL088

السأن المستدان

DNA sequence: (SEQ ID NO: 67)

ATGTCCAATGACAACGAAGTACCTGGTTCCATGGTTATTGTCGCACAAGGTCCAGACGATCAATACGCATACGAGGTTCC CCCTATCGATAGCGCGGCGTTGCCGGGAATATGTTTGGCGACTTGATTCAAAGAGACATATATCTACAGAAAAACATTT GGCTTGCTAAAGCAGATCACTCAAGGAAAAAGGGAGGCCACAAGGCAAGAGCGAGTCGATGTCATGTCGGCAGTCCTGCA TCTCCATCTATGAGGCCTGGGTCAAGATCTGGGAGAAGAACTCTTGGGAAGAAGAAGAAGAAGAACCCTTTTCAGCAGCTT GCTCAACAAGCAAAAAGCGCTAAAGGAAAAAGAGGACCTCTCTCAACTGGAGCGGGACTACAAAAACCAGAAAGGCGAATC TCGAGATGAAAGTACAATCCGAGCTTGATCAAGCGGGAAGTGCTTTGCCTCCATTGGTCAGTCCAACGCCAGAGCAATGG GAATGCCCCAACCCTTAGAAAAGCAGAAAGCCATCTACAATGGTGAGCTACTTGTGGATGAGATAGCCAGTCTACAGA AAGAGCCTTGAGAAATTTAGCAAAGGCTTTGGAGTTGTAGGCAAAGCTATTGACGCCGCCAGCCTGTACCAAGAGTTCAA GATATCTACGGAAACCGGGGACTGGAAACCATTCTTTGTAAAAGTTGAAACACTAGCTGCTGGTGCGGCCGCCAGTTGGC GCGATGATTGACGAAGGCCTTCTAGAAAAAGCAAACAACCTTGTAATGTCCATTTAA

Figure 30 12

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FIGURE 30M

Protein sequence: (SEQ ID NO:189)

MSNDNEVPGSMVIVAQGPDDQYAYEVPPIDSAAVAGNMFGDLIQRDIYLQKNIYYPVRSIVEQGTKEKKEINKKVSDQVD GLLKQITQGKREATRQERVDVMSAVLHKMESDLEGYKKTFTKGPFIDYEKQSSLSIYEAWVKIWEKNSWEERKKYPFQQL VRDELERAVAYYKQDSLSEAVKVLRQELNKQKALKEKEDLSQLERDYKTRKANLEMKVQSELDQAGSALPPLVSPTPEQW LERATRLVTQAIADKKQLQTTNNTLIKNAPTPLEKQKAIYNGELLVDEIASLQTRLDKLNAETTRRTEAERKAAEEQAL QDAVKFTADFYKEVTEKFGARTSEMAHQLAEGARGKNIRSSAEAINSFEKHKDALNKKLSLKDRQAIAKAFDSLDKQMMA KSLEKFSKGFGVVGKAIDAASLYQEFKISTETGDWKPFFVKVETLAAGAAASWLVGIAFATATATPIGILGFALVMAVTG AMIDEGLLEKANNLVMSI.

RL089

DNA sequence: SEQ ID NO: 68

ATGAACCGTCCACGCCTGGTTAATCGTACCTCCGCGACACCTTCGACGCTTCTGCAGCGGGCTATCTTCGACGGCTACGA CTTCGGCTTGAAGATCCCCTACATCGCAGGCAGCAATCGCGCGCTGCTGGAGCTGTCCGGCTTCTTCATCAGCGCCCGGG AGCATCCGTTGCACCGCTACTGGCGGGTCCCCAAAGGCAAGCTGCTGCCTGAACTGGACACTCTGTACAACCGTCTCGCC GAGCTAGCTGGAGGCCTTCACTCCCAGTCCTGGCGGGAGTTCAGCTCCTTGGTCGAATCCGCGCAGGCCTCGCTTGACCG ACAGGCCTTCACCTGGGGGATGCTGCTGCGCATCGCGCCCCTGGCCGAGGGCGCGTCCTACTGTCAGGCGAGTTCCATC CTGGTGTTGTGGCGGTGGCTCGGCGGATGCGCGGGGTATTCCTGCGCCCATCGAGTTCCTGGCGCATCGACACCACTCCC GAGCTGCTCCGAAGCAACCTGATTCTGGAGCTTGGCCTCGCCGAGGAACAATTCGAGATTCTGGATACTGTCCAGGAGC**T** GCTCAGCGACGGCAGCTTCGCGCCGTCGACCGAGCTGCCCAGCATGAGCATCGGCGGTCCACAGCAGGAACCGGCAGCAG CATCCTGGAGGACGAGTCAGCCTCTGACATCTACCTCGCCGCGGTGCCGGAGATCGAGCGCACCGAGTACAGCTCGGCT GATATCGAGGCGGCGCTTCAGGGCTACTCTCTACTGGCCCACCAGCCTGACGGCATCGCTCATCTGCTGCAGAGAACCAG CAATCCTGGTCATCACCCTGGCTACCCTGCTGATCAATTGGCAGCGGGAGATCCAGGAGGTCTATCCCTCGGCCACCGTG GCCATCCAGCAGGACACCCCAGAGGCGCAGTGGATCCTCGTCAACTACGAGCAGTTGAGCCCCTTCGTCGCCAACGCTTC GCGCTTCGCCGTGATGGTCATCGACGACGGCGCAGCGGATGAAGGAACCGACGGCGCAATGCACGCGCACGGTTTCGACA TTGCCGCCCAAGTGCCGAACCGCTACCTGCTTACCGGCACGCCGGTGCTCAACCGCGAGACAGAGCTGCACACCCTGCTG CGCCTCTCAGGCCACCCCATCGGCCAACTGCCGCTGAAAGAGTTCTGCGACCGTTTCGCCGGCAACCCGGAGTTCCGCCA GAGTCTGCGGCGGAGCTGGGTGACTGGATGCTGCGCAGGCGCAAAGATGTGCTGCCCAGCCTCAAGGGCAAGCAGCGGC GCGTCACGCTGGTGGGCAATGACTCGCTCACCAAGCGGCAGAAGGCGATAGATCGCTTCCAGCAGGATCCCGACTGCCGA GTGTTCATCTGCACTACGGCGGCCGCAGGGACGGCCAACAACCTCACTGCGGCGAACTACGTGTTTTTCCTCGGCCTGCC CTGGACTCCCGGTCAGCAGGAACAAGCCGAAGACCGCGCGTACCGAAACGGCCAGCTCCGCATGGTCGTGAAAATCC CACTGGTCGAGGCCACGATCGACGAGCAACTGTGGCAACTGCTCAACGCGAAACGCCAGGTTGCCCAGGACCTCATCGAG CCCGAGCAGGTCGACGGAAACCGCGCGCTTTTAGCCGCAAGCCTAACTGGATAA

Protein sequence: (SEQ ID NO: 190)

MNRPRLVNRTSATPSTLLQRAIFDGYDFGLKIPYIAGSNRALLELSGFFISAREHPLHRYWRVPKGKLLPELDTLYNRLA ELAGGLHSQSWREFSSLVESAQASLDRQAFTWGMLLRIAPLAEGGVLLSGEFHPGVVAVARRMRGVFLRPSSSWRIDTTP ELLRSNLILELGLAEEQFEILDTVQELLSDGSFAPSTELPSMSIGGPQQEPAAPSLEDESASDIYLAAVPEIERTEYSSA DIEAALQGYSLLAHQPDGIAHLLQRTSALLADDMGLGKTRQAVIAASIRAAGRPILVITLATLLINWQREIQEVYPSATV AIQQDTPEAQWILVNYEQLSPFVANASRFAVMVIDEAQRMKEPTAQCTRHGFDIAAQVPNRYLLTGTPVLNRETELHTLL RLSGHPIGQLPLKEFCDRFAGNPEFRQSLRAELGDWMLRRRKDVLPSLKGKQRQLLKVALSTEERQQYDVLRLEDRPVFA RLGALRRYLETVKVRVAMDLLSELDAEDKVILFCEFKPTVAALKELCEQAGHGCVTLVGNDSLTKRQKAIDRFQQDPDCR VFICTTAAAGTGNNLTAANYVFFLGLPWTPGQQEQAEDRAYRNGQLRMVVVKIPLVEATIDEQLWQLLNAKRQVAQDLIE PEQVDGNRALLAASLTG.

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FIGURE 30N

RL090

DNA sequence: (SEQ ID NO: 69)

CGTCGCCAACACCTGGGCAACACATTTCTCCCTCGCAGGGACAGCTCGAACCAAGTTCATCCGTCACTACCTGCGCAGCA CATCTACGACCAGGTGCTGGTGCATCACAGTCGCTGCTGACAACGGTGTGCGTTACACCATCATGCGTGCAGGGCCGCTA CTCCAGGTATTCGACGGTCAACTAATTGGTGCGTGGGAGTGCAAGCCTGCCCATCGTATCCCGGCAAGCACGCCGTCTCG AGCAGGGGCCTTGAAGCTGCTACAGCGCCTTCAAAAGTTCGACGACGCAGTTGCTGTACTCAGCTCATACACAAAGCGAG GCCGGCTGCAAATGCTGAAGGCTCAGCCGGTCTTGACGCCGCTACTGGTGGATTGCGAGGAGGAGTCTGGCCTCACACG CGCCGCCATGCCATGCGACTTGTACCTCGATATGGGCCGTATTCTTGGGCAGGTCGCGGACGAAGGAATTTCGGTCATCA ACTTTTTCGCCTGGCTATTTCAGGCGCCGCGGGCCTCGATTCGATTTCTTAGTCACGTCAGTCCCGGCCGTGCGGGAGGA GCTCTCTTCCATCGCAAACGGGAAGGCCGACATTCGGGATGGCATGCTCTCCTACTGGCGGCATCGCTAGGTAACCGGCG GCCGATCACTCGCGCTCAATGGACAGCATTCTATGCCGCCTACAATGCGATCCCTTGGCAAGTTCACAACGCCAAGCCCG -ACTACAACCGTCTCTTCAACGGCTGCCCGTCGGATTGGCAGGATCCGGCATGGCTTGCAATCACTGCACGGCTGAGAGAC ATCAAGGAGTTCTATACCGCCCTCGACCAGGGGAACTCACAGGTTGTTCGGCAGGCGCGCAGCGCCCTGAAAGCGTATCT GGGTCATTGTACCTACCGACAAGCTGGCAACCTGGTGGACGACTACCACCAGGTCCAGAGGGAGCTGCCGCAGTGC CCTAATGGACTGCAGATCGTCGAGCTCCGCTGTCCTGCCGACCTATATGCCGAACATATCGCTCTGGCACATTGCATCGA TAGCTACGACCAGGCCGCCTACCGAGGAGACTGCCGACTGCTCTCAGTACGTGAGGCTGGTCGTCCGCTGGCCTCTGCCG GAATTCGATAATGCCCCCGTGCCGACCGACTCGCCTGCCGGCCAGGCATACCGCTGGTTCATGGAACGAATTCGCTCTGG AGCCATAGCGACGAACCTGAACTGGCCCGACATGACCGTCCACATGACGCGCTTCGCCAATGGTCGCTGGAAGGCGGGCC TCGCCGAAGCCACGGCGAAGTGGCTGCTCACTCAGTTGGAAGACCGATGA

Protein sequence: (SEQ ID NO: 191)

VAPLDNAPPSGPLQDPSLARYSERQLAVANTWATHFSLAGTARTKFIRHYLRSTSTTRCWCITVAADNGVRYTIMRAGPL LQVFDGQLIGAWECKPAHRIPASTPSRAGALKLLQRLQKFDDAVAVLSSYTKRAHDLATQMARDDLGLQHRLVYPSHSNK RYYAPRHQFYLKQIGAVLRTFRQVLDQDLLFAIRSVRCLSPQLYNWLAQGDQVRRLQMLKAQPVLTPLLVDCEEGVWPHT TTNDNGESIRHYLPCFFPQLDSERPQAAAMPCDLYLDMGRILGQVADEGISVINFFAWLFQAPRASIRFLSHVSPGRAGG ALFHRKREGRHSGWHALLLAASLGNRRPITRAQWTAFYAAYNAIPWQVHNAKPDYNRLFNGCPSDWQDPAWLAITARLRD IKEFYTALDQGNSQVVRQARSALKAYLGHCTYRQAGNLVDDYHQVQRELRAAVQSSLPDLVDTDEYTTWEGMLSVGLIDC PNGLQIVELRCPADLYAEHIALAHCIDSYDQAAYRGDCRLLSVREAGRPLASAELELRREHGEPIGRPWSPKHLSTVQLR EFDNAPVPTDSPAGQAYRWFMERIRSGAIATNLNWPDMTVHMTRFANGRWKAGLAEATAKWLLTQLEDR.

RL091

DNA sequence: (SEQ ID NO: 70)

Protein sequence: (SEQ ID NO: 192)

 ${\tt MRKENISAEITERAFDFFYWFSRFEFSLKENGYLKNYKPGARAEPGWENFVQNHSDKYSLSQSATALIEQSPEQQIVLPG} \\ {\tt RELGWRPVKLDEDKSDLARVARLLKTVRNNLFHGGKHGGANWDNPARTIHLILLSKAILDEFAALGDFEADYKRIY.} \\$

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FIGURE 30 O

RL092

DNA sequence: (SEQ ID NO: 71)

ATGCACATCGTAATCATTGAAGCCCCGGGCAAGCTGAAAAAGCTGAGGTCCCTTCTCCCCTCGATTCGTCCCGACGTGAC TGGGCCAGGATTTCAAACCGCACTACCAGATCCTCTCGGGCAAGGAAAAAACCGTCGCACGGCTGAAGGAGCTGCGGCAG GATCAAGAACTACAAGCGCGTTGCCTTCAAAGAAATCACAAAGTCATGCATCACCGCCGAACTCAGCTCGCCGCGTCGCC CGGCGCGTGATGGGTAGGCCGACCACCGCCGGGCGCGTGCAGTCCGTCGCGGTGTACCTGGTGGTCCTGCGAGAGCGGGA GATCCGCGCCTTCACAGCAATCAAGCACTTCGGGGTGGAACTGACCTTCGTTTCGCCCAGCGACGGCCGTACCTGGACGG CGGAATGGGATCCAGTGCCCGTGTTTGCCAGCGAGGAGTTCCCGTATGTCCAGGATCGTCAACTCGCAGAACTGGTGGGG GCTATACGTAATGTCATCGTCGAGACCTGCATTGATAGCGAAGAAACCGATGCGCCTCCGGCACCGTTCATCTCCTCCTC GCTCCAGATGGCCGCCGGGAATGCGCTGAAGTGGTCACCCGACAAGACGATGAAGGTCGCCCAGCGGCTGTATGAACAGG GGCTCATCACCTACCACCGGACGGACAACCCCAATATCTCGAAGGACTCGATGCCGGATATCCGTGCTGTCGCCAAAGCC TTGGGGCTGAAGTGTTGAGCAACAGCGGATGTTCAAAGCGGACCAAGACGCCCAGGAAGGCCACCCCGCCATCACCCC TACCGACTGGATGGCCGCTGCCGCCGGTGAAACTGCTGATGAGCAGCGCTGTACCAGCTCATTCGAGTCCGCGCGCTTG TTCGGCGCCAAAGGGAAGCTGTTGAACGTGCCTGGCTGGAGAAAACTGCTGCAGGTGATGACGCCGAGGAGCAGAAGAA CGAAACGCCTTCAAACCCCATCCCGATCCCGGCGCTGGAGCCACGCCAGATACTCAAGGTCTACAGCGGCGAGGTCCTGG AGAAGAAAACCACCCCTCCCAAGCGATTCACCGACGCCAGCCTGGTGGGCGAGATGAAGCGCCGGGGATTGGTCGGCCA TCCTCCTACGCCTCGATCGTGAAGAACATCATCGACAAGGGCCAGGTGCAGATGAAGGGGCGAAGCCTGATCCCCGGCGA GCTGGGAGAGGCCACCATCGCGCTCCTGGAGCACAACTTCAGCTTCCTCAGCCTCGACTTCACCCGCAACCTCGAGGTCG CAGACACTCCGCGCGCTCCCCAGCGCACAGGACGAACCACGCGCAAGCTCCACCGCCAGTATCTCCTCGGCGCCGACCAG $\tt CGACTTCCTTTGCGGCAAGTGCGGTTTGCCCCTGGTTCACCGCAAGAAGGCGGCAAAGGCGGCTTCGACTTCTGGGGTT$ CTATAG

Protein sequence: (SEQ ID NO: 193)

MHIVIIEAPGKLKKLRSLLPSIRPDVTWQVEATAGHIRDLPVHGQDPQMLTVGVGQDFKPHYQILSGKEKTVARLKELRQ KAVEIYVASDPDREGESIGWHILQAAGIKNYKRVAFKEITKSCITAELSSPRRLDLPKVASQECRRVIDRLVGYLVTPEL RRVMGRPTTAGRVQSVAVYLVVLREREIRAFTAIKHFGVELTFVSPSDGRTWTAEWDPVPVFASEEFPYVQDRQLAELVG AIRNVIVETCIDSEETDAPPAPFISSSLQMAAGNALKWSPDKTMKVAQRLYEQGLITYHRTDNPNISKDSMPDIRAVAKA LGLKCVEQQRMFKADQDAQEGHPAITPTDWMAAAAGETADEQALYQLIRVRALASQIEAAVYAVRTITLLGVGPDKKPLR FGAKGKLLNVPGWRKLLQGDDAEEQKNETPSNPIPIPALEPRQILKVYSGEVLEKKTTPPKRFTDASLVGEMKRRGIGRP SSYASIVKNIIDKGQVQMKGRSLIPGELGEATIALLEHNFSFLSLDFTRNLEVALDRIANSEDTYMNVVQQFYQLLQTEL QTLRALPSAQDEPRASSTASISSAPTSDFLCGKCGLPLVHRKKAGKGGGFDFWGCSGYRTTGCKVSYPTKSGRPDFDNPRG L.

RL093

DNA sequence: SEQ ID NO: 72

ATGGATCAAAGCCTTTGCACATGCATGCCAACGCCAATCGTCAACCCCAAGGAGCTGCGACTGTGCCACATGTTAGTCGG TAGAACTTTCCCGATAACATTGATCGCAGGCGACCATTGGTTGAGCTATGACGGCAGCGCCTGGTGGGTCGATGCGGATG AGCCCGCGACGGAGGACGAGGTGGCGGCTCTGTTGGTCAAGGCTGGTGGTGCTCACTACGTGCTGGTGCGGATAG

Protein sequence: (SEQ ID NO: 194)

 $\verb"MDQSLCTCMPTPIVNPKELRLCHMLVGRTFPITLIAGDHWLSYDGSAWWVDADEPATEDEVAALLVKAGGVTTCWCG".$

RL094

DNA sequence: SEQ ID NO: 73

GTGGCAAGGGCTTCCGAATCGGAAATCTCGACCAGTACGAGGTGCAGTGTGTCAAAGAGAGCGACCGATACCGACAAGCT GGACAGACGACACTTCAACGATCCCCACCGGACTGTACGGGCTATTGGTGCTGAGGCCGCGGGAAAGGGCTACGGGTGT TCGACTGCCCCTACAGTCATCCTGCGATGCGGGCGTCCTGGTTGAAAGGGTTTGCCCAGGAGCAGCAACAGCAGCTCGAC TTCTGA

Protein sequence: (SEQ ID NO: 195)

VARASESEISTSTRCSVSKRATDTDKLDRRHFNDPHRTVRAIGAEAARKGLRVFDCPYSHPAMRASWLKGFAQEQQQQLD

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FIGURE 30P

RL095

DNA sequence: (SEQ ID NO: 74)

ATGGCTACCCCGTCTTCTGGGAAGCCAACATTGGCTCGGCGCGCGGAGCACCGCAGCTTCCCCAACGGCAACAATCCCCC
GCGGCAGTTGCTGCGACTGAACGTGATTCTCGACAACTCGATTCCCGATGGCCAAGGTGGCTACAAGGATCGCGGCGGCT
TCTGGTGCAGCGTCGAATGGTGGCATCAGGATGCCCAGCGCTTCGCCGAACTGTTCACGAAAGGTATGCGCGTCAAGGTC
GAAGGCAGGGCCATTATGGACCGCTGGCCGGACAAAGAGTCAGGCGAAGAAGATCCAGGCGCTGAAGGTCGAAGCCTCGCG
CATTTCCATCCTTCCGCATCGCCTGGCCGAGGTCACCCTGTTGCCAACCCAGCATCAACAGTCTCGGAACGTCCCGCAGC
AACCTGCTCAGCAAGATGCGCAATCGCAGCAGGACTACGACGACGACGACGACGACATCCCCATGTA

Protein sequence: (SEQ ID NO: 196)

MATPVFWEANIGSAPEHRSFPNGNNPPRQLLRLNVMFDNSIPDGQGGYKDRGGFWCSVEWWHQDAQRFAELFTKGMRVKV EGRAIMDRWPDKESGEEVQALKVEASRISILPHRLAEVTLLPTQHQQSRNVPQQPAQQDAQSQQDYDSAFDDDIPM

RL096

DNA sequence (SEQ ID NO: 75)

ATGCGGCAGCTCGATAAGGACCAGCAAGGCGCTCTGGAACAAAGTGCCTTCCGCCCACTGCAACAAACTGCCTTCCAGGC
GCTGCAACACGTGCCTCACTAAAAGGCCTTTTAAAGCTTTTAAAGGTAATAGGGAGCTGGCCCAGTTGGCGGAACAGT
--GCGAAGCCATGGAGCAGGGATTGGTTGAACTTGCCCCAGGGACTGCTCGCCGCAGCACCCTTCACTG
CCCACCCGACCATCGAGCAGCGCACATCCGCCCGCACACCCTTTCTCCGCTGGCAGCACATTGCATCCCGGCGGATAGGG
CGTCGGGGTGTGGACGGAAATGCTGCGCAGAACACCCCGGAATACCTGCAAGACCTCTACGAGATGGAGCTGC
AGCGCATCACCCTCAACATGCAGATCAGCCTGATCCACTCATCGGCAAGCCAGGCCGCGAGTGCGCGGAAAAGATGGGC
CAGGCCGAGGCCGAGTTCATGGGCCGACTGCAGCAGAGCACCAACCCACTGA

Protein sequence: (SEQ ID NO: 197)

 $\label{thm:model} \begin{minipage}{l} MRQLDKDQQGALEQSAFRPLQQTAFQALQHSASLKGLLKPFKGNRELAQLAEQCEAMEQGLLELAQGLLAQVRRPPFTLL\\ PTRLIEQRTSARTTFLRWQHIASRRMGVGVWTEMLRQDKTPEYLLQDLYEMELQRITLNMQISLIHSIGKQAAECAEKMG\\ QAEAEFMGRLQQSTNHH\\ \end{minipage}$

RL097

DNA sequence: (SEQ ID NO: 76)

Protein sequence: (SEQ ID NO: 198)

MAETHRLQIGSLRSDVALTLHTYHAARIWTGRQKSDAKHSILGLSGFCAYVNRMHRGAAQDDPYSDWWLVQIEEKVESCQ AALEAIDQRLDDVMAKLPATLDISENLSVTPVKVPLFISNPLGFKAVYLLTNYDELARRILLAQHVGLVGRRDMEVWLDE GASVLRSLFGLAQSYQFSGATRDDFAANNARAEAARKMYEKFGEIPQDILEGTRRSNFAPPITRGRSDGDADDDADRVEL ED

RL098

DNA sequence: (SEQ ID NO: 77)

ATGTTCTTGAGCATGGCCCCTTTCTTTTTGGTCGTTCTTCTTCTGCACTTTTTACAGATGCGTGGAACGACCGAGA ACTCAGGCTGTTGATATGCTGATCGTTTCGGGTATTCAGTAACCGTGTTGACCATTACGGTTGAGATGTATCGCTTTG AAATGGCGGAAAAAGCGATGTGGGGGAGCTTTATGCAACAAAGCCAACTACATGAACTGCCAACCAGATTACCAACGGTAG

Protein sequence: (SEQ ID NO: 199)

 ${\tt MFLSMAPFFLVVLVLSALFTDAWNDRELRLLLMLIVFGYSVTVLTITVEMYRFEMAEKAMWGALCNKANYMNCQPDYQR.}$

RL099

DNA sequence: (SEQ ID NO: 78)

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FIGURE 30Q

Protein sequence: (SEQ ID NO:200)

MRKSRSGVVFFGDAARITLPGPDLRAAGELGDSTGITPPGADLRAAGELGDSTGITLPGIHFGIGGKMGVSGRNTSPKRG ITTHEELKQCS.

FIGURE

RL100

DNA sequence (SEQ ID NO: 79)

ATGAGGCTGTCGCGCTTTCCCATTTCGACACTGCTGGACTCGGCCTCGGGGCATCTCGAGGCCCATTTGTATAAGAAGCG GCTTGCTGCCGAAAGCGGCGAACCGCTGGCTCAACAATATTCCGGCATCATTTTCAGCGGCAATCCTCATGAAACCGTTC CACGGCGCCTCCTCGGATAAGCGTCTTACTCCGCTGGAGCGGAACTGCTGGCAAGTTTTCCGCTTGCTCAACGAC GACGGACTGACCGCGTTCCCGACATACGAGCAACTGCGCCCCTATCTCGGTATGCAGCCGGGCAAGATCGCCTCGCGCGA AACCATCGCCAAGGCACTCACGGTCCTTCGTCTGACCCGCTGGCTCAGCCTCGGCCGACGCCTGCCCAACGACCTCAACG GACAGGTCCAGGGCAACGTTTACATCCTTCACGACGAGCCTGTCTCTCCAGCCGAAGCCTTGGAGCTGGACACCGACTAC ATGCAGTTGCTGAGCCAATCCACCGGTCACGGCAACCGAGCCATACGCGAAATCGGGCAGATCATCTGGCGGGAGTTCAG GGATGATCCGGACGTGGGTCGCCGCCTCCCTACCCATCTGGAGAAGCTCGAGGGACGCTTGAACCACCAGCAATGGGCTA TCGATAGTCAGCTCGAAGCGGATCCAGCGGCAGAGTTCGGCATCCGAACTCTGTCGGATTTACCTCATTCCACCCCGAGT TCGGATGCCGAACTCAGTGAAATCAGCGGCAAGCAATGCGCTCTACCGCTGAGTTCGGATACCGAACCCCGACAGAATCC GCAGTAAGCGCGCTCAGACGGGTGTCCGAGGATCTTCGGCTACCCATCATCGAGCAGTGGCAGCACCGTTGTGCCGGCGG CGGAAGAACCGGCTGAGCGAACCATCCCCGCAACGGAACGCCCCATTCGTGCTCCGGCACCATCAAGCCCCCATAGCGCCT ACACAGCCTCAGGTCCAGCCCCGGGGGGATACCCGGACAGGGAGCGAGGTCCTCAGCCGGCTCAAGGACCTCATTCGGCC CAGGCACGGATCGAGCGTGCCATCCGAGCGGGGTGATGATTCATGA

Protein sequence: (SEQ ID NO: 201)

MRLSRFPISTLLDSASGHLEAHLYKKRLAAESGEPLAQQYSGIIFSGNPHETVPRRLLLDKRLTPLERNCWQVFRLLIND DGLTAFPTYEQLRPYLGMQPGKIASRETIAKALTVLRLTRWLSLGRRLRNDLNGQVQGNVYILHDEPVSPAEALELDTDY MQLLSQSTGHGNRAIREIGQIIWREFRDDPDVGRRLPTHLEKLEGRLNHQQWAIDSQLEADPAAEFGIRTLSDLPHSTPS SDAELSEISGKQCALPLSSDTEPRQNPPSTPLVRMPNSYSTYTYKQDSVCKKPVQPRAREEAHPNWQDLLHALEAEQRIQ AVSALRRVSEDLRLPI I EQWQHRCAGGTVSNPFGYLMTLI QRAVQGKFNASWAPEEPAERTI PATERPI RAPAPSSPI AP TOPOVOPRGDTRTGSEVLSRLKDLIRPRHGSSVPSERGDDS.

RL101

DNA sequence: (SEQ ID NO: 80)

ATGTCGAAGTCGACGATCAATGAAGCGGTCCTGACGCAGGTGCTCAACCACCTGCGCAACGGCCAGCTCAGGCGTTGTGC $\tt CGAGATGGGGCTGCGGAGATTCTGGCTCAGCTCCAACAGCCTGCCGTCATGAGCATCCTGACCAATACCCCGGTTT$ CCTGGGTAGATGTCAGAGTGAACATCGACGTCATGGAGAAAATCCTGGCCACAGCCGAGCGCAGCGCGCAGGAAGACCTG CAGATCGAACGCGCACTGAAGCTGGGAGCCACCACAACGATGATCCAGAGCTTTTTCGGTCTGTCGCCGGAGGACACCGC GGTTCCGCTGGGAGCACCTGATGCAGGAAAATCAGGTCCGCCTTGAAGACAGCATGGAGTTGCTGGACATCGCGATGATC CTCACAGAGGAAATCAACGCCGGAATCGAACAGACAGTCCAGAATTCATCAGCCTCGCCATTGTTTTGGTCTCTCATCCA CAGCTGGTTGAAAGACGGGCTCTATCCGTCTGGCAAATCGAGCCAGAGCCAGGCGGGCCTGCAAAAGTCCCAATCCACTC TTTACCTCGCTAGCGTCAGCTCACACCTGCCCCACTCTGCCCCATCCGCAACAACGCAGGTGAACGCTGAGACAGAACGT CAACAACTACTGAACCTGGTTCAGTCGGAAGGCGACACAGCACCATGA

Protein sequence: (SEQ ID NO: 202)

MSKSTINEAVLTQVLNHLRNGQLRRCAEMGLRPEILAQLQQPAVMSILTNTPVSWVDVRVNIDVMEKILATAERSAQEDL QI ERALKLGATTTMI QSFFGLSPEDTATKRLMLE I HPRRGRWRQLDEQI ERQI WFRWEHLMQENQVRLEDSMELLDI AMI LTEEINAGIEQDSPEFISLAIVWSLIQSWLKDGLYPSGKSSQSQAGLQKSQSTLYLASVSSHLPHSAPSATTQVNAETER QQLLNLVQSEGDTAP.

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FIGURE 30R

RL102

DNA sequence: (SEQ ID NO: 81)

ATGAGTATGGCCAAGATCAACCCGCAAGATCTGAAAGACCGGCTACTTGCCCCTGGTTTTACCGCACCGCCCAAGGTTCT GGACCACTCGAAACCCGAAATACGATGAGCTGAAAGAATCGATCCGACATCGAGGCCTCGATACGCCGCCACCAGTGACT CGACGCCCTGGAGAGGACAAATACCGCATTCGCAACGGCGGAAACACTCGCCTGGAAATTCTCAACGACCTCTACAAAGA GACCGGAGACGAGCGCTATTTCAGCTTCGACTGCCTGTTCAAGCCCTGGGACAAGCAGCGCGGCGAAATCATCGCGCTGA ${\tt CCGGTCATTTGGCCGAGAACGATCTGAAGGGCGACCTCAAGTTCATCGAGCGCGCGGTTGGGGTGCAGAAGGCGAAATTT}$ CTTTACGAACAAGAGAACGGCGGTGAAAGCATTTCCCAGCGCGAGTTGGCACGTCGGCTAAAAGCGGACGGCTACCCTGT TCGGTAAACCGCAAATCGAGAAACTCCTGTCACTCAGAAAGTCGGCATCCTCCTGCTGGGCACGTCTATACGCTGGTGAA GGGGTTGACTTCGAAATGCTGTTCCAGGACACCCTGGCAATCTTCGACAGTAGCCCTGACGAATTCATTTTCGAGCGTTT CCAGGACGAACTCATCGACCAAATGAAGCGCCCCCTGGGCCTGCGTTATGACCAAATCCTGCTCGAGATTACCAACGGGC AGCAGGAGCAACGCCGCGGCACTCTGGTCGACCTGCCCACACTCCCGCCACCTCAACTCCCACCAATTGGGCAGGAA AACCCTGCTGCGTCTACTGGACAAGCACAAACACAGAGCCCCGCCGCAGATCCCCAAACGTCCAGGACAAGGAGCAA CCCGGGTAATCCCCTCCCCCGCCGCCGCCACCACCTGTCCAACAAAGCAATTGCCCGATGAGGAGCGTGCGGCGG CATCTACCTGTCTTCGATGAAACAGCTCTGCAGGCAATCCCAGTGCAAGTCGGTGGCCTGCACCCGATCACCGATCTCTG GTACATCGAGEGGTCGATCGATACCCCCGAGATCCTGCGACAGCACATCGCTGATCTGGCTGAAGAGATCGCTCTGCATG ${\tt TCGGCGCCCAGGCGAGATCGTCAGGATTCAGGGCGGTGTGGGTTACACGTATCGCGAGCCCAATGAAGACCATGAGATT}$ ACAGACCTGCCGCGATGCACTGGGTGAATTCCAGTTCTCAGCTGGCCTCGCTCAGTTGCTGGGCCAACCCACAA GTGACAAGCCATCCTGCCAGGCAGGCCGTCTCAATGACGAAGCCCTGGTGAAACTGTTCCGGATCATTCGTCTTGCCCGA

Protein sequence: (SEQ ID NO: 203)

MSMAKINPODLKDRLLAPGFTAPPKVLEOLSDPISDTPMRLTLHDVLPWHDNPRTTRNPKYDELKESIRHRGLDTPPPVT ${\tt RRPGEDKYRIRNGGNTRLEILNDLYKETGDERYFSFDCLFKPWDKQRGEIIALTGHLAENDLKGDLKFIERAVGVQKAKF}$ LYEQENGGESI SQRELARRLKADGYPVSQSHI SKMLDTI EVLAPAI PVMLYSGLGKPQI EKLLSLRKSASSCWARLYAGE GVDFEMLFQDTLAIFDSSPDEFIFERFQDELIDQMKRPLGLRYDQILLEITNGQQEQRRGTLVDLPTPAAPPQLPPIGQE NPAASSTGQAQTQSPAADPQTSRTRSNPGNPLPPPAPPPPVQQKQLPDEERAAVLAGHIVSPVSTKIQQTRQRLAGLEGE HLPVFDETALQAIPVQVGGLHPITDLWYIERSIDTPEILROHIADLAEEIALHVGAPGEIVRIOGGVGYTYREPNEDHEI TDSALHLMTLLQAVSGQVQVVLNTHDQQTCRDALGEFQFSAGLAQLLLGQPTTSDKPSCQAGRLNDEALVKLFRIIRLAR RLVDLELPPAASEQAATDQ.

RL103

DNA sequence: (SEQ ID NO: 82)

GAGCAAACCGAATGGTCGACGAACTCTTCGCCAAGAACCAGCGCCTGCAGGCTGAGCTGGCGGCGGCGAACACGCCTCAG GTGGCGGAGGCATGA

Protein sequence: (SEQ ID NO: 204)

 ${\tt MTMARETEDKFVVRMPLGLRDQLKQKAADNHRSANSEIVYRLERSNALEEELARANRMVDELFAKNQRLQAELAAANTPQ}$ VAEA

RL104

DNA sequence: (SEQ ID NO: 83)

CGAGCTGGGCGACTCCCAGGCCATCGAGAACCTGCTGGCCGACCTCAACGAAAGCTACAACGCCAAGAACAAGGCCTGGG ${\tt GGCTTCAGCCGCGAAGCGGTCGAGCACCTGCAAAAGCTGATGGAGGAGTCCAATCTCTTCACCGGCGGCCACGTCCTGTT}$ CGCCCACTACCAGCAAGGCATGACCGACTACCTGGCGATCGCCCTGCTGCACCACAGCGAAGGCGTGGCGGTGAACGAGT CGCTGGAGGTCACCCCGTCGCCACCTGGACCTCGGCCAGTTGCACCTGGCCGCGGGATCAACATTTCCGAATGGCGC AACAACAAGCAGTCGAAGCAGTACATCTCGTTCATCAAGGGCAAGGGCGGGAGGAAGGTCTCCGACTATTTCCGCGACTT CATCGGCTGCCAGGAAGGGGTGGATTCGCCGAGCGAGACGCGCCCCTGCTGAAAGCCTTCAGCGATTTCGTGGAAAGCC AGGACATGGCCGAGGAACAGGCCCGCGAGAAGACCGAGACGCTGGTCGACTACGCCACCTCGCAGGCGCGCATCGGCGAG CCGATGACCCTCGACGCGCTTTCGGAACTGATGGACGACCAGCAGCGCGGGCGTTCTACGACTACATCCGTAACAAGGA CTACGGCCTGTCGCCGGAAATCCCGGCGGACAAGCGCACCCTCAACCAGTTCCGCCGCTTCACCGGCCGCCGCAAGGCC TGTCGATCAGCTTCGAGGCGCACCTGCTGGGCTCCAGGATCGAGTACGACGAGGAGCGCGACACGCTGCAGATCAGCAGC CTCCCCACTCAACTCCGCGACCAGCTCAAGCGGCGCAAGGCCCAAATTGGAGAATGA

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FIGURE 30S

Protein sequence: (SEQ ID NO: 205)

MPIKHAIVHLIEKKPDGTPAVLHARDAELGDSQAIENLLADLNESYNAKNKAWGFFQGESGAYPFSGWLGEYLEGDRDFV ${\tt GFSREAVEHLQKLMEESNLFTGGHVLFAHYQQGMTDYLAIALLHHSEGVAVNESLEVTPSRHLDLGQLHLAARINISEWR}$ $\verb|MNKQSKQYISFIKGKGGRKVSDYFRDFIGCQEGVDSPSETRTLLKAFSDFVESEDMAEEQAREKTETLVDYATSQARIGE|$ ${\tt PMTLDALSELMDDQQPRAFYDYIRNKDYGLSPEIPADKRTLNQFRRFTGRAEGLSISFEAHLLGSRIEYDEERDTLQISS}$ LPTQLRDQLKRRKAQIGE.

RL105

DNA sequence: (SEQ ID NO: 84)

ATGCGTAGTTTCCTTCGCGGCGCCCCGGGAAAGCGTTCGCCGGCTGGTGGCCTTCGCTCAAGCAGAAGGCTGGAGCGTCGA GCGGCGAGCTCAATGCCCGCGCCCTGCTCCGTCGAGCCGACAGGCAGCGTTCCCTGAACCAGGAGTCTTTCTGA

Protein sequence: (SEQ ID NO: 206)

 ${ t MRSFLRGARESVRRLVAFAQAEGWSVDRSAGGHLKLSKIGCASIFISSTPSDARGELNARALLRRADRQRSLNQESF$

DNA Sequence: -(SEQ ID NO: 85) ${\tt ACACGGTCGCGGTCACCTGTCGCGTCAACGGCACCAGTAGCAACTGACGGTATGCACTCAACTGCGCACAGAGGTCCG}$ CATGCTGCGTTCCGCGCATGACGACCTGGCCTGCAGCCGGCAGAGCGATCGTCGCAGCCTTCAGGCGCTGGTGAAACGTC TCCTGGATGCCGCCGCCGCTCCCTTCCCCGCTCCCTTGCAGAGATGGAGACCTGGCTGCAGCTCAACAGCGAGGAG ACCACGAATGCGTAG

Protein sequence: (SEQ ID NO: 207)

MPDVTAYRPLEHFQKVELMLELKLREGPSWICLNCGYHLDGSGAQPCPDCGKSRYWTSGWSVGRGHRFSAAREEWENRLR ${\tt TRSRSPVASTAPVATDDVCTQLRTEVRMLRSAHDDLACSRQSDRRSLQALVKRLLDAAATDSLPRSLAEMETWLQLNSEE}$ TTNA.

RL107

DNA sequence: (SEQ ID NO: 86)

GTAGCGCGCGATGCCTGA

Protein sequence (SEQ ID NO: 208)

 ${\tt MKASQTYQCIVKFDGAGFWINTIQKQRATCTWSDKVAASRLAERLFGEDNAYITRMPVQAGDHEKRIESRWALSCRNPKE}$ VARDA

RL108

DNA sequence: (SEQ ID NO: 87)

ATGAACACTGAAGCCCGCTTTCCGAGTATCCACGCCTCGGCCGCGTTCACCGACTCGGCAGTGGTTCATGCCAATCACGT TGGGGTCAACCCCATCGAGCTGGACGCCCTCAGCCAAGTGATCTCGCGCGCTTTCGCGGGACGAGAGCACGGTCGCACCCA GTTCGATGGAGCGAGGGCTTCGTGAGCTGGAGGAACTGGGGTACATCGAAATCTCGACCACCCAGGCCGGGACTCTGGTG GTCACTACGCGCGCTCCGGGGCAATTGCTTTCGGCTTACTTCTGGTCGGTATGGATCCCGCGACACCTGTTCAGCTGCTC GCTGAAAGTGAGCCTGGTGCCGCACCTCTGCTGCGGCACTCAGGACTCCCAGCACCTCACCGCGTGTTCCGCATTGCAG GCAGCAAGGACGCCGCGCGAGTTCCTGCATCAGTTGGCCAACAACTATCCCGGGCATGAGCCGGAGTTGCCCGAACTG GTGGCCGTTCAGGTCGGTGATGCACTCAGCAAGGAGGCCGAGTCATGA

Protein sequence: (SEQ ID NO: 209)

 ${\tt MNTEARFPSIHASAAFTDSAVVHANHVGVNPIELDALSQVISRLSRDESTVAPSSMERELRELEELGYIEISTTQAGTLV}$ VTTRAPGQLLSAYFWSVWIPRHLFSCSLKVSLVPHLCCGTQDSQHLTAVFRIAGSKDAAREFLHQLANNYPGHEPELPEL VAVQVGDALSKEAES.

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FIGURE 30T

RL109

DNA sequence: (SEQ ID NO: 88)

GTTTCTGCAGATCAGCCGGGAGGACTCGAAGTGAGTGTTCTGGAACTTACGCCGCCGCACTCCGTCGAGGCGGAGCAAGG ${\tt GGTACTCGGCGGCCTGATGCTGGACAACGCGGCATGGGACATTGTCGGCGATCAGTTGCAGAAGGAGGACTTCTTCCGGC}$ ATGAGCATCGGCTGATCTTCACCGCCATCAGCGAGTTGGCCGCGAAGGATGCTCCGTTTGATGTCGTGACTGTCGCGAA ${\tt GCGATCGAAGACCTTCCAGAAGCTGGCGGGCTGGCCTACCTCGGCCAGCTCGCCGACAACACGCCCTCCGTGGCCAATAT}$ CAACGCCGATTTCGTCGATATCAACAAGAGTCTCACGAAGATCGTCGACACCATCGATTACCGCTTCAACAACAACGTGA $\tt CGGTAACGGGGGTCCCGACTGGCCTGAAGGATCTCGACGCACTCACCGGCGGACTACAGAAGTCGGATCTCATCATCGTC$ GGTGCCCGCCCCGCGATGGGCAAAACGTCGTTTGCCCTCAACCTGGTCGACACCGCGCTCCAGAGCGACCAACAGAAGTC $\tt AGCCGGCTGGTCATCAGCGCCAACCTCACGCCGACAGGCTGCGCCCAAGGTTCGCCGGGCGGCCAGGAAGTA$ $\tt CGGACACCCCGCGCTGATATTGGTCGACTACCTGCAACTGATGAGTTGCCCAGGCCTGGAGAATCGAGCCACCGAGATCT$ $\tt CGGAAATCTCCCGCTGGAAAGCGCTGGCCAAGGAGATGGACTGTCCCGTCGTAGCTCTATCCCAGCTAAATCGCGGC$ CTAGAGAACCGGACGAACAAGCGACCGAACTGCGCGGACCTACGAGAGAGGGGCGCGAATCGAGCAGGACGCGGACGTGAT GCÄACGGTCCGATCGGCACCGTCCACACCGCCTTCATCGCCAACCAGACCCGCTTTGCCGACCTGGCGCCCGGGGACCTGG CAA

RL110

DNA sequence: (SEQ ID NO: 89)

Protein sequence: (SEQ ID NO: 210)

MTRSALSTIAYEALVRARRKFSNREERCIRETWTAEQELVLLRLYPDMPNEVLAARLNKTLQQICSRAYRLGLKKSPEFS KKIRQDWGSATRFKKGNTPWNCGMKGLPARGRAPETQFKKGQKPHTWLPVGSTRVSADGYLQRKISDTGYPPRDWKGIHI LLWEEHFGPIPTGHCVCFKDNNKQNVVIDNLELITRAERMRRNSIHRYPPELKSAIRVISKLKRTIQEVEHEEQD

RL111

DNA sequence: (SEQ ID NO: 90)

Protein sequence: (SEQ ID NO: 211)

.....

MDKQKVLAKVEKLMALANAKGATPNEAETALRQAAILKRQFDLSDAEISAHTVETACVPTRTRSPAPWLHELAGICASS FGCDYLAAYAMPAGWTFKFMGRGIGPELAAHAYSTLHHQLVAARSAHVAQQKRCKLSTKRRRSKLFVEGWLLAVRSLVRE FAGRPDESTQAAIKAYLELHHPALKYLEPAALTKALAYDQASLQAGWEHGKNTRLHRGVSRRVQGALEQGGSQ

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FIGURE 30U

RL112

DNA sequence: (SEQ ID NO: 91)

 $\tt ATGAGTGACCCCAAGCTCAAGCCCTGCCGCTCTGCGGCAGCACGAACATTCGAATGCTGGAACCCGAGCTGCTCGACAC$ ${\tt CAGCGAGGTATTCAGCACAGATCGACTGGAATAGACGCCCAAGCGCAAAAAAACCACGCGGACGAGCGTGAGCAGTTCTTG}$ $\tt ATGGCCAACCTGCTCGCCGCCCTGGAGGTCGCACTGGGCGACGTAGCAGCCCTGGCTATTGTCGATCGGGTAAGACAGGC$ $\tt CTCCATGCCGGCGGCATCGGCACCGACTGGCCGGGCGGCATTCGGAATGGCTCTGCACTGTTCTGGCCCTGGGACGAAGA$ GCTCCGCCACCGAGCAGGGGCTCAACCATCTGCAAGGGGGGGCGCGTAA

Protein sequence: (SEO ID NO: 212)

MSDPKLKPCPLCGSTNIRMLEPELLDTDAWNCAIECLDCQVHIGPSYCEPDPVTARYSAQIDWNRRPSAKNHADEREQFL MANLLAALEVALGDVAALAIVDRVRQATDRIYPTSNLSPVPQAWLDVQAERRRQITVEGFDTSNDDASAGLIALAAGCYA $\verb|LHAGGIGTDWPGGIRNGSALFWPWDEEWWKPKSARENLVRAGALVLAEIERLDRSATEQGSTICKGGA|$

RL113

DNA sequence: (SEQ ID NO: 92)

 $\tt ATGAACCTCCAGAACCGCAACAACCTCCTACTGAGCTTGATCGCCGAGACCCAGTTCGACGCCTACGTGCAAGGCTACAT$ GGCCAAAGCAGGCGCTGCCGCCGGTGCTTCCGAGAATCTGCAAATCGAGGCTGAAGGTGCTGCGATGTTGCAGGGCCTGG TCGCTCCGGTTCGCGCTCAGCAGCGTGCCTGTGGACAGTCCCTGCAGAACGCACTGCTCCAAATCGCCCACGACCTACTG TTGCAGACGAAATCGCAACTGGCCATCGCGGCCAATGCCAGTTCGATCCAAGTGATCCAGCGGGACATGAACAGGGCGAT $\tt CTGGAACATAGCTACTGCCATCGATCACCTGGCCGAGTTCGCCCAACCCTCGCAGGACACTGTGAGGGTCATCGAACGGC$ TGATGCTCTTCGTCGGCAGCTCATCAAGCACTGAAGGCCAGCAACTGGCCGCCGAGGCAAATGCGGTGCTCGGCATGAGC GTGGGAGGCCTGGCATGA

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Protein sequence: (SEQ ID NO: 213)

MNLQNRNNLLLSLIAETQFDAYVQGYMAKAGAAAGASENLQIEAEGAAMLQGLVAPVRAQQRACGQSLQNALLQIAHDLL LQTKSQLAIAANASSIQVIQRDMNRAIWNIATAIDHLAEFAQPSQDTVRVIERLMLFVGSSSSTEGQQLAAEANAVLGMS VGGLA

DNA sequence: (SEQ ID NO: 93)

CGCGCTTGCTCGACTCGGTGAACAAGCAGATCGAGCATGCGAAGGAAAAAGCCGTGATCGCTACGAGAAAAAAGCCAAGAAG ${\tt GCTGGAAATCCTGCAGATCGCGTTGATCTACAACCGGGCCAGGGTGTTCGATCACCTGTACTCCACGCACCAGCTCCACT}$ CAAAACTCAAACGCTGGCTGGAGCGTCCAAAGCAGCTCATCGGATGGCGCAGTGAAGCCGAGTATTTCGCTAGTCAGGTG $\tt GGGAGCCTGCGATGTGACTTAGCCATCTGACTAACGAAATCGCGTACGACGATGGCAGTGAAGTCGAGGAGCGCCT$ ${\tt GCGCGTCATCAAGCAGAAGGTCGCTGACTGCACCGCACAGATCGCTCTGACCAGCGAGGAGCAGGAAACCCTTCGGCTCT}$ GGACAGACGCTCTGCAATCGGCTCCGGAGGGCCTCATATGA

Protein sequence: (SEQ ID NO: 214)

 $\verb|Lnkfgsaadlrsqqakltgatreirkltgggidlfgklgcylsfeqkqllqdaarlldsvnkqiehakekrdryekkakk|$ RRELRERLAKQLVASNYPLPGNTLEDRLEILQIALIYNRARVFDHLYSTHQLHSKLKRWLERPKQLIGWRSEAEYFASOV GSLRCDFISHLTNEIAYDDGSEVEERLRVIKQKVADCTAQIALTSEEQETLRLWTDALQSAPEGLI

RL115

DNA sequence: (SEQ ID NO: 94)

ATGAATGCGAAAGCGACTTCGGTTGTATCCACCAAGGGTGGTGTAGGAAAATCCACCACCGCCGCCAACCTCGGTGCATT ${\tt CGGAAGTTGCCCAGGGGGGGATTTACGACCTGCTCGCCGCCAACATAACGGACCCGGCGAGGATCATCTCCAGGACGATT}$ ATCCCCAATCTGGACGTCGTGATTTCCAACGACCAGAACAATCAGCTCAACAACCTACTGCTCCAGGCGCCCGATGGCCG GCTACGCCTGGCGAACCTGATGCCCGCTCTGAAAGAAGGCTACGACCTGGTGCTGATCGACACCCCAGGGTGCGCGCTCAG CTTTGCTCGAAATGGTTGTGCTTGCATCGGACCTGGTTGTTTCCCCCCTCCAACCCAACATGCTTACCGCCCGTGAGTTC AACCGCGGCACCATGCAAATGCTCGACGGCCTACGCCCCTATGAGCGTCTCGGCATGCGGATCCCCAATGTTCAGATCGT TTTCTGTGCTCGAAACGACTGTCCCGGATGCCGTCGTGTTTCGCAACGCAGCGCGCGGGCTACCAGCGCACCGCCTC GAAACGCGGCAACCCTCCAATCGCACATCAGCGCCCGCGCTGGAAATCATTCGAAACCTGGCCATCGAGGTCTTTCCCGA TCCTATCACCCAAGCCCGCGACGTCGACGCGGAACTTGTGCTGGAACTGA

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FIGURE 30V

Protein sequence: (SEQ ID NO: 215)
MNAKATSVVSTKGGVGKSTTAANLGAFCADAGIRTLLIDLDPVQPSLSSYYELPEVAQGGIYDLLAANITDPARIISRTI
IPNLDVVISNDQNNQLNNLLLQAPDGRLRLANLMPALKEGYDLVLIDTQGARSALLEMVVLASDLVVSPLQPNMLTAREF
NRGTMQMLDGLRPYERLGMRIPNVQIVINCLDQTNDSRAIHENVRAIFDEHQDISVLETTVPDAVVFRNAASRGLPAHRL
ETRQPSNRTSAPALEIIRNLAIEVFPEWTDRFLALTPGGGCSTGQGRALTWRRLLSPKPATSTRNLCWN

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FIGURE 31A

RS01

DNA sequence: (SEQ ID NO: 95)

RS02

DNA sequence: (SEQ ID NO: 96)

--ATGACGCCGCAGCAGCTCACCGAGGAGTACATCTTCGCGCACGATCTCCGAGAGAGCCAGCGCGAAGATCTACCGCGCGC GACCAAGGCGCTGCTCAAGCACTTCGGCCCTACGGCAACCGTACAGGAGGTGGACCACAGGTCTGTGCTGGGATGGCGGC ${\tt GCAAGGTCCTGGAACAAGGCCTGTCGAAGCGGAGCTGGAACACGTATTCGAATCATCTGCGAACGATCTGGGGCTATGCC}$ AACCGTCGCAGCCGAAGCCATCCTGCGCGCCCGCAATTGGCTCAACATGCAGGTCGGCGCCGAGCGCTGCACTGGCGATC GCGCACGCATCACTCCCGCCTGGTTCTGGCTTTGCACGTTTGAGGTCTTCTACTTCACCGGCATCCGGTTGAATGCGCTG TTGTGCATCCGCAAGCGCGACATCGACTGGGAAAATCAACTGATCCTCATCCGCGGGGAGACAGAGAAAACTCATAAAGA GTTCGTAGTGCCAATAACGGAGGGGCTTGTGCCTCACCTATCGCGGCTCCTGCAGGAGGCCGATAGAGCCGGATTCGCCG ATGACGACCAGTTGTTCAACGTCAACCGGTTCTCACCGCACTACAAGAGCAAGGTGATGAACTCCGACCAGGTCGAAGCC ATGTACCGGAAGTTGACCGAGAAGGTTGGGGTGCGGATGACTCCGCACCGTTTCCGGCACACCCTGGCCACCGACTTGAT GAAGGCACCCGAGCGGAACATCCACCTCACGAAGTGCCTGCTCAACCACTCGAATATCCAGACCACCATGAGCTACATCG AGGCCGACTACGACCACATGCGTGCCGTGCTGCATGCCAGAAGCCTGGCCCAAGGAGCGCTGGAGAACGTCAGGAAGGTG ACAGGAGGCTAGGACAGAACCTGCAGAACCAAGGGAGCACACCCAGGGACAGGCATTCAGGGAGATGCAACCGCGTGGG AAGAAGCGCTACCACAGCCACCTGACACCTTCGAGCAAAGCGTGCTGTTCACTCTGATGGCTCAACACCTATCGAACCCT GCCGCCACGGCCTCCGCGGCTTCCACCGCAACAAGCGGATCTGGAGGATGGGGATCTACCGCCCGAAGCAGTCTCGCCTA

Protein sequence: (SEQ ID NO: 216)

RS03

DNA sequence: (SEQ ID NO: 97)

ATGAAATCTGGTATCGCGACCCGTCGCCTGTTCATCAACGACACCAAGGCTTTGGTGCATACCGTCGACGGGACCGCCAT GCTGGTCACGCCAGGAATCTTCAAGCGTTATGTCCAGGAGCATCCGGAGGTTGAAAAGCTGGCCCAGGCCAAGGAGACCG CCGGCTGGAAGCTGGTGCAGCGCGCGTTCGAGAAACAGGGTCTTCACCGAAAGACCAGTAAGAACCTGAATATCTGGACC ATCAAGGTTTCTGGTCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGTGCA GCCTCTGGACAACCCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Protein sequence: (SEQ ID NO: 217)

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MKSGIATRRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPEVEKLAQAKETAGWKLVQRAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPVQPLDNPSLTVITDAEGGVE

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FIGURE 31B

RS04

DNA sequence: (SEQ ID NO: 98)

ATAGACCAGTTGAGTGAGCAGGAGTCGGTGAAGTGGTCTGCTCAGCTTTCGATGTGGCGCGGGTCTTGCTACTACGTCCA
CCGTCTTCGACGGCGGCGTGTCGATGCTCGCCGCGTGGCGCTACGCAGCCAAGTCAACCAGTTGTTCAGCCAGAGTCGGG
GCTCGGCCGGCAGCCGCAGCATTCTGGGCATGCTGCGCGCAAGAGAGGGCGTGACCATCGGCCGTTTCCGAGTGCGTCGGTTG
ATGCGTGAGCTGGGCCTGGTCAGCAAGCAACCGGGCTCGCACGCCTACAAACAGGCCACGGTTGAGCGGCCGGATATCCC
GAATCGGCTGAACCGCGAATTCGCCGACCGAGCATCCCCATACAGGTGTGGTGTGGCGAACTACCCTACGTCTGGGCGCAAG
GCCGTTGGCACTACCTGGCCGCGTGCTGGATCTGCTGATCGGCTTGAGGCGTTCCATTCAGACCAGGACTGCTG
ATCAAGGCCCTGGATGGCCTACGAACAGCCGGCAAGCAGGAGAGAGCATTCCATTCAGACCAGGGCAGCAGTA
CGCCAGCCGCCTGTTTCGGCAACGGCTCTGGAGTCGGATGCAGCAGAGAGCCGTCGGGGGAATTGCTGGGATA
ACTCGCCGATGGAGCCCTGTTCCGCAGTCTGAAGTCGGAGTGGGTCCCGTCAACGGGTTACCTGACGCGCAGGAGGCC
CAACGGGACATCAGTCATTACTTGATGCACCGCTACAACTGGATCAGGCCGCATCAATTCAACGACGGGTTACCACCTGC
GGTGGCCGAAGAAAAAACTCAACCCACTGTCCGGGATGGGTTGG

Protein sequence: (SEQ ID NO: 218)

IDQLSEQESVEVVCSAFDVARSCYYVHRLRRRRVDARRVALRSQVNQLFSQSRGSAGSRSILGMLREEGVTIGRFRVRRL MRELGLVSKQPGSHAYKQATVERPDIPNRLNREFATEHPIQVWCGDITYVWAQGRWHYLAAVLDLLIGWAFSAKPDAELV IKALDMAYEQRGRPQQVLFHSDQGSQYASRLFRQRLWRYRMQQSMSRRGNCWDNSPMERLFRSLKSEWVPSTGYLTAQEA QRDISHYLMHRYNWIRPHQFNDGLPPAVAEEKLNPLSGMG

RS05

DNA sequence: (SEQ ID NO: 282)

ATGAGCAAGCACGTACGTTTTCCGCCGAGTTCAAACGAGAGGCCGCGGCCCTGGTGTTGGACCAAGGCTACAGCCA
TATCGACGCCTGCCGTTCGCTGGGGGTGGTGGATTCGGCCTTGCGCCGTTGGGTGAAGCAGCTCGAGGCGGAGCCCAGG
GTGTGACCCCGAAGAGCAAGGCGTTGACGCCTGAGCAGCAAAAGATCCAGGAGCTGGAAGCCCGGATCAACCGATTGGAG
CGGGAGAAAGCGATATTAAAAAAAGGCTACCGCTCTCTTGATGTCGGACGAACTCGATCGTACGCGCTGA

Protein sequence: (SEQ ID NO: 219)

 ${\tt MSKQRRTFSAE} {\tt FKREAAALVLDQGYSHIDACRSLGVVDSALRRWVKQLEAERQGVTPKSKALTPEQQKIQELEARINRLERKAILKKATALLMSDELDRTR}$

RS06

DNA sequence: (SEQ ID NO: 99)

Protein sequence: (SEQ ID NO: 220)

 $\verb|MLYFSCSMKMGGWVGYRYFSLFSLIALIYGCVGGGGGSDEIGQHCFEREQKLSGVNDNEEGSVRLNRLNCDPIEGRVLES|\\ EKLIRKPPNELGIH|$

RS07

DNA sequence: (SEQ ID NO: 100)

Figure 31 2

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FIGURE 31C

Protein sequence: (SEQ ID NO: 221)

MKKSLVMSAVLLVASNFACADEGSNDGSEICRAQGGVEITSLGEVSKGVDVEDVVVCSILPSNMKSSQRAPTLPPLQRMI ISAMPSPGTVTVSASGDRKFTTSCRANLYAPRYANFYPDGVSRGTSDLRCVGYNTPGNSSQGCNVSWDGPTDIQLGVEPY GGSVVVNYSCTAFKTTIPVIMSYSYRDGRAVYGEVQNVSGIINVVLN

RS08

DNA sequence: (SEQ ID NO: 101)

ATGCTTATTAAAATTCTTCGAATTATATTCTTGTTGCCTATAGTTGGCTTGGCACAGCAGGCTGCTGCCTCCCCGCCGC
AGAGTCACACTCGGAACAATCTGAATCTTCGTGTATCGATGTCCAAGTCAATGGAGCACGTAGCCTGTCTTATAACTGCA
TGGCTCAGCAAATGACTCCACCCAAAGAGGATCCTCGGCGTCGGAACCCTACCTTGAACTCCACATTAGCGTCTGAACGC
GCCACTCGCCTGCCACCCACACAGACAGGACTTTTTACCAGCCTTCATCAACGTGCCATATCGAACTCGAAAGACTAG

Protein sequence: (SEQ ID NO: 222)

MLIKILRIIFLLPIVGLAQQAAASPPAESHSEQSESSCIDVQVNGARSLSYNCMAQQMTPPKEDPRRRNPTLNSTLASER ATRLPPTQTGLFTSLHQRAISNSKD

RS09

DNA sequence: (SEQ ID NO: 102)

Protein sequence: (SEQ ID NO: 223)

VSSTKSKPIARGRGGPFGEVMKRCGLVPVRGRNRQQTGSLAMGQQETISPSVSRTAACSVRGDSLMP

RS10

DNA sequence: (SEQ ID NO: 103)

Protein sequence: (SEQ ID NO: 224)

MERLLESIYINARPAMELRLSLTSSGRKRMVKIVDGEEVEVLPGEVQGILEAQKRDVGILADFLAKSLVARR

RS011

DNA sequence: (SEQ ID NO: 104)

Protein sequence: (SEQ ID NO: 225)

MECHVRPATŠRDAAAISCVVIAALRESNSQDYPPDVIAQVEQSFSPEAITTQLTKRRVFVALLGENIIGTAGLDGDVVRS VFVDPAHQKGGIGRHLMDVIHTTAASAGVGAVRVPSSITAERFYTALGYQKIRDEFHGAERTIVMEKRL

Figure 31

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FIGURE 31D

RS12

DNA sequence: (SEQ ID NO: 105)

Protein sequence: (SEQ ID NO: 226)

LWLTCTPQQDVQAALATASILLGQFHQLGVQLGRYTSLDPLEEVEKNASALPSPAWKTDSTKFSVVLKSGGRSIDKGIPT AGLLAHVMVAKFADHLPLYRQEKIFGRAGLAIARSTLAQWVGQTGVRLQPLVDALREAVLNQGVIHADETPVQMLAPGEK KTHRAYVWAYSTTPFSGLKAVVYDFSPSRAGEHARNFLGDWNGKLVCDDFAGYKAGFEQGITEIGCMAHARRKFFDLHVA NKSQLAEQALHSISGLYEVERQARDMSDEERWRIRQELAVPILKKLHDWMLAQRDLVPNGSATAKALDYSLKRWVALTRY LDDGAVPIDNNQVENQIRPWALGRSNWLFAGSLRSGKRAAAIMSLI

RS13

DNA sequence: (SEQ ID NO: 106)

Protein sequence: (SEQ ID NO: 227)

MVRRRRVAVARECLSLSSAPNQVLSMDFVFDALSTGRRIKCLTVVDDFTKVSVDILVEYGISGFRVTRALDEMARFRGYP QAIRTDQGPEFTGKALDQWACQRDIKLKLIQPGQPTQSAFIESFNGKFRGECLNEHCSLVEARIRIAAWRDYNEHRPHSA IGNLSPAELAAKWRTNQQQLKREKLISTP

RS14

DNA sequence: (SEQ ID NO: 107)

 $\tt GGGCCGCGGCAGATCACTCTGCGCCAGTTTGAGAACGGAGTCACCGAGCTACAGCTCAGTCGGCCACCATTGACCAGTCT$ GGTCCTAAGCGGCGGTGCTGCCAAAGGTGCGGCATACCCGGGAGCAATGCTGGCGCTAGAAGAGAAAGGCATGCTCGATG GCATCCGCAGCATGTCCGGTTCGTCCGCTGGCGGCATCACCGCCGCCCTTTTGGCCTCAGGTATGAGCCCGGCGGCGTTC AAGACCCTTTCCGACAAGATGGATCTTATTTCGCTGCTCGACAGCTCGAACAAGAAGCTGAAGCTGTTCCAACACATTAG $\tt CAGCGAGATCGCCGCATCGCTGAAAAAGGGCTTGGGCAACAAGATCGGCGGCTTCTCTGAGTTGCTCAATGTACTCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCCAATGTACTCCAATGTACTCCCAATGTACTCCAATGTACTCCAATGTACTCCCAATGTACTCAATGTACTCCAATGTACTCCAATGTACTCCAATGTACAATAATGTACAATGAA$ CACGCATAGATTCGCGGGCTGAGCCCCTAGAACGCCTATTGCGCGACGAGACACGCAAGGCCGTGCTCGGACAGATCGCT ACGCATCCAGAGGTTGCACGCCAGCCGACCGTTGCCGCCATCGCCAGCAGATTGCAGTCCGGCTCCGGAGTCACCTTTGG CGATCTAGATCGGTTGAGTGCTTACATTCCCCAGATTAAGACGCTGAACATCACAGGTACGGCCATGTTCGAGGGGGCGTC ${\tt GGAGTGTTCCAGAAGGTCAGCTTGAGTGATCAGCCGTACCAGGCCGGCGTAGAGTGGACAGAATTCCAGGATGGCGGGGT}$ GATGATTAACGTGCCGGTCCCTGAGATGATCGACAAGAATTTTGACAGCGGGCCCACTGCGGCGCAACGACAACCTGATCC GAAGAGCGAGCGGGTGATTTCAGTGGCATGCTCGGTGGCACCTTGAACTTCACCATGCCGGACGAGATCAAGGCGCATC TTCAGGAGCGCCTCCAGGAGCGAGTCGGTGAACATCTGGAGAAACGTCTTCAGGCCTTCAGAGCGTCATACCTTCGCTTCT

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FIGURE 31E

Protein sequence (SEQ ID NO:228)

MHIQSLGATASSLNQEPVETPSQAAHKSASLRQEPSGQGLGVALKSTPGILSGKLPESVSDVRFSSPQGQGESRTLTDSA
GPRQITLRQFENGVTELQLSRPPLTSLVLSGGGAKGAAYPGAMLALEEKGMLDGIRSMSGSSAGGITAALLASGMSPAAF
KTLSDKMDLISLLDSSNKKLKLFQHISSEIGASLKKGLGNKIGGFSELLLNVLPRIDSRAEPLERLLRDETRKAVLGQIA
THPEVARQPTVAAIASRLQSGSGVTFGDLDRLSAYIPQIKTLNITGTAMFEGRPQLVVFNASHTPDLEVAQAAHISGSFP
GVFQKVSLSDQPYQAGVEWTEFQDGGVMINVPVPEMIDKNFDSGPLRRNDNLILEFEGEAGEVAPDRGTRGGALKGWVVG
VPALQAREMLQLEGLEELREQTVVVPLKSERGDFSGMLGGTLNFTMPDEIKAHLQERLQERVGEHLEKRLQASERHTFAS
LDEALLALDDSMLTSVAQQNPEITDGAVAFRQKARDAFTELTVAIVSANGLAGRLKLDEAMRSALQRLDALADTPERLAW
LAAELNHADNVDHQQLLDAMRGQTVQSPVLAAALAEAQRRKVAVIAENIRKEVIFPSLYRPGQPDSNVALLRRAEEQLRH
—ATSPAEINQAINDIVDNYSARGFLRFGKPLSSTTVEMAKAWRNKEFT

RS15

DNA sequence: (SEQ ID NO: 108)

ATGATTGATACATGGCTGGCACAGTGGGGCTTGAGACTTCCCTCGAGCAACGATGCCACGTTGCGGCTGCAACCGGCAGA
GGGACCGGAACTGGTTATGGAGCGCCTCGAGGGCGGTTGGCTTTTCGTCGTCGAGTTGGGACTTGTGCCTTCAGGGTTAC
CGCTGGGTGTGATCTTGCAATTGTTACAAGTGAACTCTCCATTCTCATCCTTGGCACCGGTGAAACTTGCGGCGGACGAT
GCCGGTAGACTTGTGCTCTGGGCTGAGGCACGTGATGGCGTTGACGATTGGATGCACTGAACCGCTTGCACGATAGGCT
GCGGGAAGGACATTCACGATTAGTGCCATTGCTAGAGCCCACGGGTGAGTTGGTTCCAGCTCAGATACAAACCAGCGCGT
TAGTGTTCGTTTGA

Protein sequence: (SEQ ID NO: 229)

 ${\tt MIDTWLAQWGLRLPSSNDATLRLQPAEGPELVMERLEGGWLFVVELGLVPSGLPLGVILQLLQVNSPFSSLAPVKLAADD}\\ {\tt AGRLVLWAEARDGVDDVDALNRLHDRLREGHSRLVPLLEPTGELVPAQIQTSALVFV}$

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Big Island: Overall Nucleotide Homology

Total 84830bp

Bp # Species, strain, gene name Accession # Evalue

/ %identity

23559-25465: X. axonopodis pv. Citri strain 306

AE011864

83%

Only stretches within the 20437-25465bp are homologous to X. axonopodis pv. Citri strain 306. A total of 1060bp, not contiguous, from this region are homologous to X. axonopodis.

33872-38412:

P. aeruginosa, PA14, pvrR

AF482691

0.0;99%

40989-46535:

P. aeruginosa, PA01, PA2128-2132

AE004640

80%

Only stretches within the 40989-46535bp region are homologous to PA01. A total of 2406bp, not contiguous, from this region are homologous to PA01.

48266-49533:

P. putida, plasmid pWWO

AJ344068

96%

83%

Only stretches within the 48266-49533bp are homologous to P. putida, plasmid pWWO. A total of 780bp, not contiguous, from this region are homologous to P. putida.

56824-58706:

P. syringae pv. maculicola, plasmid pFKN AF359557

Only stretches within the 56824-58706bp are homologous to P. syringae pv. maculicola, plasmid

pFKN. A total of 1882bp, not contiguous, from this region are homologous to P. syringae.

64748-649 42 :	P. aeruginosa, PA103, exoU,	U97065	1E-85/96%
82447-85179:	P. aeruginosa, PA01, PA0984-0985	AE004531	0.0/97%
85334-855542:			3E-80/94%
93200-93317:	P. aeruginosa, PA158	X73064	7E-50/98%
108075-108610:	P. aeruginosa, SG17M, plasmid pKLC102	AF285416	0.0/91%
100119-101054:	P. aeruginosa, PA01, PA3849,	AE4802	0.0/98%

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Small Island: Overall Nucleotide Homology

Total 10848bp

Bp#			E value
	(Species, strain, gene name	Accession #)	/ %identity
		·	
877-1632:	P. aeruginosa, PA01, PA0977	AE004531	0.0/94%
877-2603:	P. aeruginosa, SG17M plasmid pKLC102	AF285416	0.0/92%
2978-6471:	P. aeruginosa, PA01, PA0978-81	AE004531	0.0/99%
7035-7999:	P. syringae pv. maculicola, plasmid-pFKN	AF359557	83%
Only stretches	within the 7035-7999 bp are homologous to P. s	yringae pv. maculico	la, plasmid pFKN.
A total of 534	bp, not contiguous, from this region are homologe	ous to P. syringae.	
7999-8284	P. aeruginosa, PA103, exoU,	AF27291	E-136/96
8000-8080:	P. aeruginosa, PA01 intragenic region	AE004531	E-18/91%
8120-8259:	P. aeruginosa, PA01 intragenic region	AE004531	E-24/85%
8272-8860:	P. aeruginosa, PA01 intragenic region	AE004531	E-176/88%
8470-11724	P. aeruginosa, PA103, exoU,	AF27291	0.0/99%

FIGURE 34A

RL015 **RL007** RL013 RL011 **RL003** RL001 RL009 **RL005** ORF ID Strand Left end 15,725 13,847 13,102 9,757 6,887 5,436 2,449 878 Right end 16,066 13,452 14,191 12,180 7,402 6,146 4,368 1,202 pseudogene length (aa) OKF 113 14 116 807 236 639 171 G+C content Location (%) prediction (0) 63 48 8 60 48 51 **58** 56 Filing Date: September 12, 2003 Serial No.: Not Yet Assigned Page 75. of 118 Customer No.: 21559 membrane g inner membrane membrane cytoplasm membrane membrane cytoplasm membrane ınner ınner ınner outer inner and Gene name parEHypotherical protein stabilization protein Agrobacterium tumefaciens parE C58 Hypothetical protein Hypothetical Plasmid Hypothetical Hypothetical Hypothetical Appothetical Hypothetical Gene function No significant similarity No significant similarity PA1939 / P. aeruginosa PAO1 No significant similarity No significant similarity PSPT00831 / P. syringae pv. PA0977 / P. aeruginosa PAO1 (gene name / species strain) Protein with the highest E-value (% identity) 2E-69 (30) 3E-45 (91) 8E-22 (45) E-180 (52) XAC2196,XCC3121, Proteins with lesser Cut off 30% GenBank accession no. AAK87104 AAG05327 AA054371 AAG04366

Title: VIRULENCE-ASSOCIATED NUCLEIC ACIDS AND PROTEINS AND USES THEREOF

Applicants: Laurence Rahme et al.

FIGURE 34B

RL031 RL033 **RL025** RL029 RL027 RL019 RL023 RL021 **RL017** 27,356 28,024 26,585 23,138 25,048 19,915 19,044 17,466 29,967 28,329 27,595 26,971 25,932 23,581 20,199 19,262 18,404 980 493 89 385 <u></u> 79 128 294 312 147 94 72 **57** <u>ရ</u> 47 8 2 57 S S Filing Date: September 12, 2003 Serial No.: Not Yet Assigned inner membrane membrane cytoplasm cytoplasm membrane membrane membrane outer as membrane majand membrane cytoplasm cytoplasm Title: VIRULENCE-ASSOCIATED NUCLEIC ACIDS AND PROTEINS AND USES THEREOF membrane inner ınner ınner outer Customer No.: 21559 Hypothetical protein Putative(type) effector/Hopy protein, w/ Hypothetical proteins 1 Hypothetical protein Applicants: Laurence Rahme et al. Hypothetical protein Hypothetical Hypothetical Hypothetical protein protein Hypothetical Hypothetical Hypothetical Hypothetical Hypothetical of 118 | RSRTO0869v/P/symngaepv PSPT008794/P syringae py No significant similarity No significant similarity C54 / P. aeruginosa C PSPTO0862 / P. syringae pv. tomato DC3000 PSPTO0860 / P. syringae pv. No significant similarity XAC2271 / X. axonopodis pv. PSPTO0858 / P. syringae pv. PSP00849 / P. syringae pv. omato DC3000 mato DC3000 mato DC3000 Page 76 00(69)4E-29 (50) 1E-09 (38) 1E-90 (62) 2E-48 (74) 2E-23 (55) E-125 (72) XAC2283, STY4576 AAM37124 AAN62148 AA054397 AAO54395 AAO54393 AAO54384

Title: VIRULENCE-ASSOCIATED NUCLEIC ACIDS AND PROTEINS AND USES THEREOF Applicants: Laurence Rahme et al. Filing Date: September 12, 2003 Serial No.: Not Yet Assigned Page 77 of 118 Customer No.: 21559

RIV048	RL047	RLO46	RL045	RUM	RL043	RUU O A 23	RL041	RU040	RL039	RL 038	RL037	Ruojo	RL035
	'		-	, A			•		+		+		•
50(08//	47,849	97,103	46,836	(a)	45,282	(fp. 148)	41,343	(10) Sapr	39,898	(D)	35,364		31,590
50,340	50,083	147/849	47,101	40,665	46,028	5298	42,689	41,315	40,593	99,898	36,563	OF CE	32,240
85	744	240	pseudogene	8.4	248	<u>870</u>	448	228	231	1,080	399	01	216
. 50°	65	ф	55	Đ	65	(00)	63	QJ	59	φ	59	90	62
cytoplasmi	nner membrane	membrane.		ecouter and membrane and a second periplasm.	outer membrane and periplasm	souter in membrane in and in a	outer membrane and periplasm	outer membrane and periplasm	cytoplasm	initality in the	cytoplasm	imen membrane	inner membrane
				cupD!	cupD2	cupis	cupD4	Capas)	rcsB) Paris	pvrR		
Hypothetical protein.	Hypothetical protein	Hypothetical	Recombination	Probable ((imbrial precursor)) adhesion and continued in the continued in	Probable pili assembly chaperone / adhesion and protein secretion	Probable fimbrial biogenesis usher/ adhesionand p protein secretion	adhesion and protein secretion	Probable pilis assembly assembly chaperone adhesion and protein secretion.	regulator of two- component regulatory system	sensorjoftwo- component regulatory, system	regulator of two- component regulatory system; adhesion and antibiotic resistance	sensor ottwo component	Hypothetical protein
Nosigniticani similarity	SG68 / P. aeruginosa SG17M	RSPT0088012P Syringae pv	Transposase / E. coli (plasmid p1658/97)	PAΨ[281]P aëπiginasa]PAΦ[1	PA2129 / P. aeruginosa PAO1	PAGI 30 /F periginosaRAQI	PA2131 / P. aeruginosa PAO1	DADIBDITE aeruginasait AO	Z3476 / E. coli O157:H7 EDL933	SUEVEZZIA I S. STYAMBUSTUM DID ST.	PvrR / P. aerug VieA / X. camp campestris AT	OREIdiPaeruginostikaliai Rose/AS entericaisubsp _{ra} entericaises Typhileililaus	PSPTO0880 / P. syringae pv. tomato DC3000
	0.0 (66)	((45))(58)	2E-36 (82)	6E-66(7Z)	1E-83 (64)	000(60)	0.0 (70)	4E-65 (62)	8E-33 (39)	(4)E45(9))	0.0 (100) / 2E- 55 (34)	00(01)//35 28(02)	2E-74 (63)
	XAC2259, STY4562	XAC2260*SIIX45633		i v todovalst	STY0372	A COMISSION	STY0370				pvrR	VIESI	XAC2260, STY4563
	AAN62290	A ANOBAUMA	· AAO49572	AVG05516	AAG05517	Bar Andrews	AAG05519	Occessor	AAG57352		AAM15533 / AAM41975	A11/015532/1/GA000 503	AAO54414

FIGURE 34D

RL069 RL065 **RL057** RL061 RL067 RL063 RL059 RL053 RL051 RL049 **RL055** 64,661 60,826 58,753 56,030 53,019 56,768 54,524 51,416 50,353 67,073 65,266 63,075 59,019 66,042 58,303 56,275 52,171 55,189 53,235 50,853 pseudogene 201 749 511 229 22! 120 88 82 251 166 -68 63 8 88 ಜ 57 59 59 61 50 65 6 cytoplasm cytoplasm cytoplasm OUIGI Inembrane and as pemplasm membrane cytoplasm membrane membrane cytoplasm cytoplasm cytoplasm cytoplasm membrane membrane inner ınner outer and Hypothetical Protein Hypothetical protein 3 Hypothetical (1) Hypotherical protein Plasmid-related protein Hypothetical protein protein Hypothetical Hypothetical Hypothetical protein Typothetical Plasmid-related Iransposase Transposase Hypothetical Recombination Hypothetical XF1760 / X. fastidiosa 9a5c C77 / P. aeruginosa C PA2222 / P. aeruginosa PAO1 XAC2241 / X. axonopodis pv. XAC2243 / X. axonopodis pv. No significant similarity PP4437 / ISPpu14 ORF1 / P. ⁹P4439 / ISPpu14 ORF3 / P. C68 / P. aeruginosa C SG69 / P. aeruginosa SG17M utida KT2440 *utida* KT2440 plasmid pWW53 Transposase / P. putida SB-05(25) 2E-56 (48) 1E-54 (56) 3E-50 (53) 8E-23 (42) 0.0 (69) 7E-39 (88) 7E-09 (54) 7E-34 (51) 0.0 (90) SE-50 (52) STY4560 AAM37094 AAM37096 AAN70013 AAN70015 AAG05610 BAB59051 AAF84569 AAN62171 AAN62162 AAN62291

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RL084	RL083	RI (082)	RL081	RU080	RL079	RL1078	RL077	RL076	RL075	RLIO7/A	RL073	REOTE	RL071	R1070
			-		•		'		•		+		•	
78 589	78,064	76,73	75,396	7(48)(4)	73,906	Q. 75	72,107	711191	70,626	69/126	69,111	66880	67,663	0.00
2018/02	78,597	78,055	76,475	TE MA	74,847	7,9990	72,544	71,895	71,192	(69)905	69,377	(60)69)	68,370	97.497
£	177	Spi	359	Ta.	313		145	1,42114 e-4	188		88		235	100
1 4 64	69	(2)	55	(0)	65	(2)	68	160	58	150	57	<u> </u>	53	(0)
membrane	outer membrane and periplasm	membrane	inner membrane	outer membrane and periplasmi	inner membrane	membrane and periplasmi	outer membrane and periplasm	cytoplasmi	cytoplasm	cytoplasmi	cytoplasm	cytoplasm	cytoplasm	cytoplasm
pil02	pilP2	چ <u>ۇل</u> ىم	pilR2	<u>Şeklüğ</u>	pilT2	Salles .	pilM2							
Type IIV/Bipilus// adhesion and and and approximate a protein secretion as	Type IV B pilus / adhesion and and protein secretion	All Pase // Itype IV Bip Ilus // adhesion and and protein secretion	Type IV B pilus / adhesion and and protein secretion	TypellV/Bpills/ adhesionand and proteinsecretion/	Type IV B pilus / putative peptidase / adhesion and and protein secretion	Type (V/Bpilus) adhesion and and protein secretion	Type IV B pilus / adhesion and and protein secretion	Hypothetical protein	Hypothetical protein	Hypothetical proteina	Hypothetical protein	Hypotheticali protein	Hypothetical protein	Hypothetical protein
RHO i Stendenca subsp enterica seri Dublin	PilP / S. typhimurium (plasmid R64)	niio Sysphimurum (plasmid (c4)	PilR / S. typhimurium (plasmid R64)	PILS (Singella some tips (plasmid (Söllb-P9))	BfpF / E. coli (plasmid pB171)	shuffilm.v.v./E.Gouli(plasmid) (C64)	PilM / S. typhimurium (plasmid R64)	Nosignificant similarity	No significant similarity	XE17611/X Jastidlosaj9a5c; I	No significant similarity	sin 4595//S enemen subsp. (SG91 / P. aeruginosa SG17M	Nosignitionisimilativ
3E-15(21)	1E-06 (34)		4E-51 (33)	SE-15(09)	8E-25 (27)	3E-65(68)	5E-04 (21)			1E-28(G2)		Anathrody,	6E-35 (40)	
SIIY4543 - 1-4	STY4544	SINY4545, btfiD/gsps: (Ulypeill)	BfpE, STY4546, XAC0697, XCC3423 (Type II), PA2676, PA3102, STY0164	(SIIXASA)	XAC2923, XCC2754, PA0396, PA0395	SIFX4550) XX(Q215]	PA4199, STY4540			XAC2296\S\\X4534 XGC2093;::34		PATRICAL SAVE STATE		
ANTO DIVIS	BAB91690	BABGIGSS	BAB91688	B	BAA84845	0.249)	BAB91693			Avail 87.05		GAID UZDIA	AAN62312	

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RL105	RU104	RL103	RL102	RL101	RU 100	RL099	RU098	RL097	RI1096	RL095	RL/094	RL093	RU/09/2	RL091	RL 090	RL089	RL088	RL087	RU030	RL085
		•				'		'		•		+		'		1		+		•
101,064	100048	99,797	98.061	97,266	95944	95,672	95,442	94,444	931905	93,421	92712	92,340	901095	89,551	87,528	85,558	89,574	83,023	1,001.0	79,916
101,297	101,0648	100,051	99,800	98,033	97/269	95,947	95;681	95,172	94/438	93,891	92/95/7	92,573	92,020	90,021	89/417	87,531	313.0	83,349		81,538
77	08938	84	579	255		91	79	242		156	81.8	77	64) 8	156	62)	657	498	108	The	540
65	64	60	58	58	90	60	46	63	60	61	59	58	62	44	600	64		40	, GG	63
cytoplasm	cytoplasm	cytoplasm	oytoplasm)	cytoplasm	cytoplasm	cytoplasm	membrane	cytoplasm	cytoplasm	cytoplasm	cytoplasm	cytoplasm	cytoplasm)	cytoplasm	cyroplasm	inner membrane	membrane	inner membrane	membrane and pemplasm	outmembra nce
										ssb			(op.4						, viffet	pilN2
Hypothetical protein	Hypotherical	Hypothetical protein	Hypothetical protein	Hypothetical protein	Hypothetical Society of the protein was a second control of the co	Hypothetical protein	Hypothetical protein	Hypothetical protein	Hypothetical (1)	Single-stranded DNA binding protein	Hypothëtical protein	Hypothetical protein	Topoisomerase)	Similar to luminal binding protein	Hypothetical protein.	DNA Helicase	Collem-like toxin (pyociniS5)	Colicin immunity protein	Type IVB pills y adhesion and and protein secretion;	Secretin / Type IV B pilus / adhesion and and protein secretion
No significant similarity	PA38494 Plaerugmosa PAO	No significant similarity	S@1024 Praeruginosa SG177Vi	ORF4 / Pseudomonas sp. B13	ORF5//Pseudomonus pp.B B	No significant similarity	No significant similarity	ORF6 / Pseudomonas sp. B13	XF17791/Ksfashtdiosai9a5C	C102 / P. aeruginosa C	No significant similarity	No significant similarity	fastidiosa 945C SII)	Riorf142 / Rhizobium rhizogenes MAFF03-01724	No significant similarity	DNA helicase / Dictyostelium discoideum AX14	PA09851 Praeriginosa PA01s	PA0984 / P. aeruginosa PAO1	M. 1539/ Scalericalsibab anemagiser, Typhi O'llis	PilN <i>l E. coli</i> K-12 (plasmid R721)
	(00)(96)		17,15,1116 (49)	2E-33 (40)	(GE) 80-Bit			7E-66 (52)	8E(59)(55)	6E-32 (53)			(cv)1(5)±4.c	5E-29 (41)		4E-28 (24)	00000	4E-55 (94)	40000	6E-84 (35)
	SIIW2463\SIIW1607		XI-1089-XI-1084	XF1782, STY4526	XXX(222085S)[X/4528]			XAC2209, STY4529	Section of the Systems	XAC22			XF0920 STIMIT2983 XF0920 STIMIT2983			PA0799	PANISO,			bfpB, PA1382 (Type II), XF1527, pefD (general secretion pathway protein)
	ANG DIABONS A		A VANOPORTO	CAD60668	CAMPORTED STATES			CAD60670	AVVII BASSIV	AAN62318			AA11865572	BAB16261		AAO51158	No.	AAG04373	Wilferth Brown	BAB12647

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	RL115	Milin	RL113	Ruffig	RL111	NULLIA OUTUB	RL109	RU1 08	RL107	RIJQ6
	-		-		•		•		•	
≝ 108,700 %	107,687	0.00	106,516	05/687	104,986	100.289	102,745	1005000	101,777	10) 220
数据源的操作085700% (第1085757%) (308) J. J.	108,616	107/620	107,013	ا (فِرْدُ وَمِالَا	105,687	(6864.0)))	104,107	102,338	102,034	100 783
38	309	100 m	165	22	233	26	pseudogene		85	
147 W	60	58)	60	(1)	64	G 0	61	(A)	60	(0)
100 Aug 184	inner membrane	dytoplasmi	outer membrane and periplasm	inner membrane	cytoplasm	o yloplasm		coropiasm	cytoplasm	Cytoplasm
	soj						dnaB			
	Chromosome partitioning	Hypothetical protein:	Hypothetical protein	Hypothetical protein	Hypothetical protein	प्राचित्र इतिमधित्रकारित	DNA replication and recombination	Hypothetical protein	Hypothetical protein	protein.
anRUP_aerugmosaiPAO1,	Soj / P. aeruginosa SG17M	ORUSOW'P Spuide plasmid	PA2226 / P. aeruginosa PAO1	No significant similarity	STY1595 / S.enterica subsp. enterica ser. Typhi CT18	ENYO875//Fuzöbagienium nudleaium sübsp vincenili 19250	Replicative DNA helicase DnaB / Pseudomonas sp. SLT2001 (plasmid pQBR55)	No significant simulation is a	No significant similarity	No significantes indicato
	1E-84 (90)	10E25(85)	2E-32 (47)		1E-16 (32)	(PP) (PARP)	E-130 (60)			
	XF1785, XAC2205, STY4521						PA4931, STY4442, XAC1477, XF0361, XCC1434			
	AAG02083	Aug nagi	AAG05614)		CAD01841	0.00	CAD13464			

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Alignment: No_2 - embl|AL039136|HSM003612

Homo sapiens mRNA; EST DKFZp566K094_r1 (from clone DKFZp566)

18 DQTCDNLSQNPPHHLLLRLLDHWGDPAGCWSLGQTYSGHLYLPYCRELHKCSLCAHRNWH SEQ ID NO: 230
DQTCDNLSQNPPHHLLLRLLDHWGDPAGCWSLGQTYSGHLYLPYCRELHKCSLCAHRNWH SEQ ID NO: 231
H: 29 DQTCDNLSQNPPHHLLLRLLDHWGDPAGCWSLGQTYSGHLYLPYCRELHKCSLCAHRNWH SEQ ID NO: 232

HYCCLWPVWMLCYMSW
HYCCLWPVWMLCYMSW
256

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Alignment: No_8 - embl|M79137|HSXT01285

EST01285 Subtracted Hippocampus, Stratagene (cat. #936205) H

Q: 75	18	QVQHPPLCLLDQHQQEC1PPCLPPDHLQDPQHPFLLPDHHVPHLVVL1QPQLCRALAP	SEQ	ID	NO:	233
. •	43	QVQHP .CLLDQHQQECIPPCLPPDHLQDPQHPFLLPDHHVP.LVVLIQPQLCRALAP QVQHPXXCLLDQHQQECIPPCLPPDHLQDPQHPFLLPDHHVPXLVVLIQPQLCRALAP	SEQ SEQ	ID ID	NO:	234 235

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Alignment: No47 - swissnew|P35555|FBN1_HUMAN

FIBRILLIN 1 PRECURSOR.//:swiss|P35555|FBN1_HUMAN FIBRILLIN 1 PRECURSOR.//:trembl|L13923|HSFIBRLLN_1 product: "fibrillin"; Homo sapiens fibrillin mRNA, complete cds. //:gp|L13923|306746 product: "fibrillin"; Homo sapiens fibrillin mRNA, complete cds.

Q:	18 CGGASCHNTLGSYKCMCPAGFQYEQFSGGCQDINECGSAQAPCSYGCSNTEGGYLCGCPP SEQ ID NO:236
Q.	GGGASCHNTLGSYKCMCPAGFQYEQFSGGCQDINECGSAQAPCSYGCSNTEGGYLCGCPP SEQ ID NO:237
	2617 CGGASCHNTLGSYKCMCPAGFQYEQFSGGCQDINECGSAQAPCSYGCSNTEGGYLCGCPP SEQ ID NO:238

GYFRIGOGHCVSGMGMGRGNPEPPVSGEMDDNSLSPEACYECKINGYPKRGRKRRSTNET SEQ ID NO:236 GYFRIGOGHCVSGMGMGRGNPEPPVSGEMDDNSLSPEACYECKINGYPKRGRKRRSTNET SEQ ID NO:237 GYFRIGOGHCVSGMGMGRGNPEPPVSGEMDDNSLSPEACYECKINGYPKRGRKRRSTNET SEQ ID NO:238

DASNIEDQSETEANVSLASWDVEKTAIFAFNISHV-NKVRIL	178	SEQ ID NO:236
DASNIEDQSETEANVSLASWDVEKTAIFAFNISHV NKVRIL		SEQ ID NO:237
DASNIEDOSETEANVSLASWDVEKTAIFAFNISHVSNKVRIL	2778	SEQ ID NO:238

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Alignment: No56 - trembl|AF088916|AF088916_1

gene: "EMI"; product: "elastin microfibril interfase located protein"; Homo sapiens elastin microfibril interfase located protein (EMI) gene, complete cds.

//:trembl|AF 088916|AF 088916_1 product: "emilin precursor"; Homo sapiens emilin precursor, mRNA, complete cds and 3' UTR. //:gp|AF 088916|5353510 product: "emilin precursor"; Homo sapiens emilin precursor, mRNA, complete cds and 3' UTR.

//:gpnew|AF 162780|6693840 gene: "EMI"; product: "elastin microfibril interfase located protein"; Homo sapiens elastin microfibril interfase located protein (EMI) gene, complete cds.

```
Q: 7 DGDVYNPSTGVFTAPYDGRYLITATLTPERDAYVEAVLSVSNASVAQLHTAGYRREFLEY SEQ ID NO: 239 DG.Y:P.TGVFTAP. GRYL::A.LT .R.. VEAVLS SN..VA::.:.GY. E LE SEQ ID NO: 240 H: 896 DGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLE- SEQ ID NO: 241
```

```
HRPPGALHTCGGP-GAFHLIVHLKAGDAV
::P .. :. G. G.F.LI: L:AGD.V
NKPVAESQPSPGTLGVFSLILPLQAGDTV
983 SEQ ID NO: 240
983 SEQ ID NO: 241
```

gene: "EMI"; product: "elastin microfibril interfase located protein"; Homo sapiens elastin microfibril interfase located protein (EMI) gene, complete cds.

//:trembl|AF088916|AF088916_1 product: "emilin precursor"; Homo sapiens emilin precursor, mRNA, complete cds and 3' UTR. //:gp|AF088916|5353510 product: "emilin precursor"; Homo sapiens emilin precursor, mRNA, complete cds and 3' UTR.

//:gpnew|AF162780|6693840 gene: "EMI"; product: "elastin microfibril interfase located protein"; Homo sapiens elastin microfibril interfase located protein (EMI) gene, complete cds.

```
Q: 7 DGDVYNPSTGVFTAPYDGRYLITATLTPERDAYVEAVLSVSNASVAQLHTAGYRREFLEY SEQ ID NO: 242
DG..Y:P.TGVFTAP. GRYL::A.LT .R.. VEAVLS SN..VA:::.GY. E LE SEQ ID NO: 243
H: 896 DGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLEN SEQ ID NO: 244
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HRPPGALHTCGGPGAFHLIVHLKAGDAV 94 SEQ ID NO: 242
. . : : G G.F.LI: L:AGD.V SEQ ID NO: 243
KPVAESQPSPGTLGVFSLILPLQAGDTV 983 SEQ ID NO: 244
```

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Alignment: No59 - pironly|A35763|A35763

unnamed ORF; P.lividus 2-alpha collagen (COLL2-alpha) mRNA, complete cds. //:pironly|A35763|A35763 collagen alpha 2 chain - sea urchin (Paracentrotus lividus) (fragment)//:gp|J05422|159962 unnamed ORF; P.lividus 2-alpha collagen (COLL2-alpha) mRNA, complete cds.

Q: 92 GENGSSGSQAPLQGLRGIFGLWGRRSRARFCGPR-PVARLGGGTSAGRELGL 142 SEQ ID NO: 245 GE G.SG...P QG:RGI G: G...:. GPR P. GGG S G.. GL SEQ ID NO: 246 718 GEPGPSGENGP-QGVRGIPGVVGENGKTGRGGPRGPPGLRGGGGSRGERGGL 768 SEQ ID NO: 247

unnamed ORF; P.lividus 2-alpha collagen (COLL2-alpha) mRNA, complete cds. //:pironly|A35763|A35763 collagen alpha 2 chain - sea urchin (Paracentrotus lividus) (fragment)//:gp|J05422|159962 unnamed ORF; P.lividus 2-alpha collagen (COLL2-alpha) mRNA, complete cds.

Q: 92 GENGSSGSQAPLQGLRGIFGLWGRRSRARFCGPR-PVARLGGGTSAGRELGL 142 SEQ ID NO: 248 GE G.SG...P QG:RGI G: G...: GPR P . GGG S.G.. GL SEQ ID NO: 249 768 GEPGPSGENGP-QGVRGIPGVVGENGKTGRGGPRGPPGLRGGGGSRGERGGL SEQ ID NO: 250

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Alignment: No60/63 - swiss|P20062|TCO2_HUMAN

TRANSCOBALAMIN II PRECURSOR.//:trembl|M60396|HSTCII_1 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II (TCII) mRNA, complete cds.
//:gp|M60396|339196 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II

(TCII) mRNA, complete cds.

Q: 8 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMAIRTVREEILKAQTPEGHFGN SEQ ID NO: 251 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMAIRTVREEILKAQTPEGHFGN SEQ ID NO: 252

H: 183 VEPFHOGHHSVDTAAMAGLAFTCLKRSNFNPGRRORITMAIRTVREEILKAQTPEGHFGN SEQ ID NO: 253

VYSTPLALQFLMTSPMPGAELGTACLKARVALLASLQDGAFQNALMISQLLPVLNHKTYISEQ ID NO: 251 VYSTPLALQFLMTSPMPGAELGTACLKARVALLASLQDGAFQNALMISQLLPVLNHKTYISEQ ID NO: 252 VYSTPLALQFLMTSPMPGAELGTACLKARVALLASLQDGAFQNALMISQLLPVLNHKTYISEQ ID NO: 253

DLIFPDCLAPRVMLEPAA 145 SEQ ID NO: 251
DLIFPDCLAPRVMLEPAA SEQ ID NO: 252
DLIFPDCLAPRVMLEPAA 320 SEQ ID NO: 253

TRANSCOBALAMIN II PRECURSOR.//:trembl|M60396|HSTCII_1 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II (TCII) mRNA, complete cds. //:gp|M60396|339196 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II (TCII) mRNA, complete cds.

Q: 8 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA 47 SEQ ID NO: 254 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA SEQ ID NO: 255 H: 183 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA 222 SEQ ID NO: 256

TRANSCOBALAMIN II PRECURSOR.//:trembl|M60396|HSTCII_1 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II (TCII) mRNA, complete cds. //:gp|M60396|339196 gene: "TCN2"; product: "transcobalamin II"; Human transcobalamin II (TCII) mRNA, complete cds.

Q: 8 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA 47 SEQ ID NO: 257 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA SEQ ID NO: 258 H: 183 VEPFHQGHHSVDTAAMAGLAFTCLKRSNFNPGRRQRITMA 222 SEQ ID NO: 259

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A'lignment: No65 - swissnew|P23142|FBL1_HUMAN

FIBULIN-1 PRECURSOR.//:swiss|P37888|FBLD_HUMAN FIBULIN-1, ISOFORM D PRECURSOR.//:trembl|U01244|HS2444_1 product: "fibulin-1D"; Homo sapiens fibulin-1D mRNA, complete cds. //:gp|U01244|1621019 product: "fibulin-1D"; Homo sapiens fibulin-1D mRNA, complete cds.

Q:	18	RNCQDIDECVTGIHNCSINETCFNIQGGFRCLAFECPENYRRSAATLQQEKTDTVRCIKS'SEQ ID NO: 260
		RNCQDIDECVTG1HNCSINETCFNIQG.FRCLAFECPENYRRSAATLQQEKTDTVRCIKS SEQ ID NO: 261
н:	521	RNCQDIDECVTG1HNCSINETCFN1QGAFRCLAFECPENYRRSAATLQQEKTDTVRCIKS SEQ ID NO: 262
		CRPNDVTCVFDPVHTISHTVISLPTFREFTRPEEIIFLRAITPPHPASQANIIFDITEGN SEQ ID NO: 260
		CRPNDVTCVFDPVHTISHTVISLPTFREFTRPEEIIFLRAITPPHPASQANIIFDITEGN SEQ ID NO: 261
		CRPNDVTCVFDPVHTISHTVISLPTFREFTRPEEIIFLRAITPPHPASQANIIFDITEGN SEQ ID NO: 262
		LRDSFDIIKRYMDGMTVGIRR 158 SEO ID NO: 260

LRDSFDIIKRYMDGMTVGIRR 158 SEQ ID NO: 260 LRDSFDIIKRYMDGMTVG: R SEQ ID NO: 261 LRDSFDIIKRYMDGMTVGVVR 661 SEQ ID NO: 262

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Alignment: 80 - trembl|AF045447|AF045447_1

gene: "DPC4"; product: "deleted in pancreatic carcinoma"; Homo sapiens deleted in pancreatic carcinoma (DPC4) gene, exon 11 partial sequence and complete cds.

//:trembl|U44378|HS443781_1 gene: "DPC4"; product: "Dpc4"; Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. //:pironly|S71811|S71811 probable transcription regulator MAD-4 - human//:gp|AF045447|2865657 gene: "DPC4"; product: "deleted in pancreatic carcinoma"; Homo sapiens deleted in pancreatic carcinoma (DPC4) gene, exon 11 partial sequence and complete cds. //:gp|U44378|1163234 gene: "DPC4"; product: "Dpc4"; Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds.

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Q: 6 PGSRIRGRVDTLQXNAPXXMMVKDEYVHDFEGQPXLXTEGHXIQTIQHPPXNRAXTETYX SEQ ID NO: 263
PG :.G TLQ.NAP..MMVKDEYVHDFEGQP.L.TEGH.IQTIQHPP.NRA.TETY. SEQ ID NO: 264
139 PGIDLSGL--TLQSNAPSSMMVKDEYVHDFEGQPSLSTEGHSIQTIQHPPSNRASTETYS SEQ ID NO: 265

TPALLAPXEXNATXTANFPNIPVAXTXQPAXILGGXHXEGLLQIAXGPQPGQQQNGFTGQ SEQ ID NO: 263
TPALLAP.E.NAT.TANFPNIPVA.T.QPA.ILGG.H.EGLLQIA.GPQPGQQQNGFTGQ SEQ ID NO: 265

PATYHHNXTTTWTGXRTAPYTPNLPHHQKG 155 SEQ ID NO: 263
PATYHHNXTTTWTGXRTAPYTPNLPHHQLG SEQ ID NO: 264
PATYHHNSTTTWTGSRTAPYTPNLPHHQLG SEQ ID NO: 265
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Alignment: No86 - trembl|D32210|D32210_1

gene: "Notch2"; product: "cell surface protein"; Mus musculus (Notch2) mRNA, complete cds. //:gp|D32210|2373395 gene: "Notch2"; product: "cell surface protein"; Mus musculus (Notch2) mRNA, complete cds.

0:	81	MPALRPALLWALLALWLCCATPAHALQCRDGYEPCVNEGMCVTYHNGTGYCKCP-GFLGE	SEQ	ID NO:	266
-	•	MP LRPA.L ALL LWLC A PAHALOCR.G.EPCVNEG.CVTYHNGTG:C:CP GFLGE	SEQ	ID NO:	267
u.	1	MPDLRPAALRALLWLWLCGAGPAHALOCRGGOEPCVNEGTCVTYHNGTGFCRCPEGFLGE	SEO	ID NO:	268

YCOHR-PCEKNRCGDPSTC 157 SEQ ID NO: 266
YCOHR PCEKNRC: TC SEQ ID NO: 267
YCOHRDPCEKNRCONGGTC 79 SEQ ID NO: 268

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Figure 44

PROTEINS AND USES THEREOF

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Figure 46

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SEQ ID NO: 113 adaptor V D K E K K K V F T L G C G T 1 S G L SEQ ID NO: 273 P G R A V G A T L A D C S P L L H L L P A I H P GGAGGTCTTCCCCCAGCACTGGCTTGTGAGGAGGTCCCTCTGCCCGGGAGAAAATGGCTCCTCCGGGTCAC AGGC 300 POHWLVRSS LCPG ENGSSG S TCCCCTCCAGGGACTGAGGGGGCATTTTTGGATTGTGGGGAAGGCGCTCCAGGGCCCGGTTCTGTGGCCCCAGGCC 375 P L O G L R G 1 F G L W G 1GTIGCTCGGCTGGGTGGAGGCACCTCTGCAGGCCGGGAGCTTGGTCTTTGAACACCT V A R L G G G T .S A G R E L G L

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Figure 49

PROTEINS AND USES THEREOF Applicants: Laurence Rahme et al.

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Figure 51

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Title: VIRULENCE-ASSOCIATED NUCLEIC ACIDS AND PROTEINS AND USES THEREOF

Applicants: Laurence Rahme et al.

Filing Date: September 12, 2003 Serial No.: Not Yet Assigned Page 100 of 118 Customer No.: 21559

Pathogenicity Island Probe #	P. aeruginosa srains that gave Positive signal with the specific probe used	P. aeruginosa srains that gave Negative signal with
(bp # ) 3 (25562-26456)	PA14, CF2, CF6, CF26, CF29	the specific probe used PAO1, PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF30, CF32
4 (61181-63607)	PA14, CF2, CF6, CF26, CF29	PAO1, PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF30, CF32
5 (74933-76117)	PA14, PAO37, CF2, CF6, CF26	PAO1, PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF29, CF30, CF32
6 (84922-86622)	PAO1, PA14, PAO37, CF2, CF, CF26,	PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF29, CF30, CF32
7 (103070-104556)	PA14, PAO37, CF2, CF6, CF26	PAO1, PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF29, CF30, CF32
8 (104799-105545)	PA14, CF2, CF6, CF26	PAO1, PAK, CF1, CF3, CF4, CF5, CF27, CF28, CF29, CF30, CF32

These experiments indicate that at least part of the big island region contained in each probe is present in the P. aeruginosa strains that gave positive hybridization signal.

Figure 53

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ORF7 Protein SEQ ID NO: 278

MINSHLLYRLSYRGTSFFQPWTLPVLLDSRLRGAPFYGCARACQPSDPKSFSSFSTSDKTALPLHAAALSRLPDAHEKAP PKRGFPCPPPKRSGEDDLVAFHLRRDTGTRREFAGQDQLRQRVLDPALDGPLQRACAIDRVEADGNQLVQRLLAQFQAQL ALGQALAQATELDLGDAGDLLASQRLEHHHFVDPVDEFRTEVRIDRVHHCGTLRLAVAGQLLDLRRTEVGGHHHHGVAEV HRTPVTVGQASVLEHLEENVEYIRMGLLHLVQQHHRVGLAADRLGQVAAFLEADVARRRADQAGHRVFLHELGHIYPHQR LLGIEEELGQRLAQLGLAHPGRAEEEERAARPVRIGEAGARTAHGVGHGDYRLVLADHSPMQLLLHAQQLLALALEHLRH RDTGPLGNHFGDFLVGHLVAQQLVLGLAVLVDHLQAAFQVRDGLVLDARHALEVALAPRRLHLLLGLLDLLLDLRRALHL GLLGLPDLLEVGV FALELDDILLQLGQALPGGFVVFLLQRLALDLQLDQATVETIQFLRLGVDLHADAAGGLVDQVDGLV RQLPIGDVAVRQLGRGDDRAVGDAHPVVHFIAFLEATEDGDGVFLARFVHQHLLEAALQRGILLDVLAILVEGSSTDAVQ LAARQSRLEHVAGVHGTFRLAGADHGVQFVDEQDDPAFLLAQFVEDRLQAFLELAAELGTGDQRPHVQGQQALVLEAVRH FAVDDALGQALDDGGLADAGFADQHRVVLGPPLQDLDGPADLVVATDHRVELAFLGALGHVDGVLVQRLARLLDVRVVHR FAATQVGHGILQRLARHALAEQQLAEPGVLVHRGQQYQLAGDELVALLLGQAVSLVEQACEILGQVHVAGRALDLRQRVE FFVEAAAQGGDIEADLHQQGLDRTALLLEQGGKQVHRLDGRMVMANGQGLGVGERQLQLAGQTVYSHGSSFLL.

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ORF7 nucleotide sequence SEQ ID NO: 119

GCCGGCGCCGACCATGGTGTGCAGTTCGTCGATGAACAGGATGACCCGGCCTTCCTGCTTGCCCAGTTCGTTGAGGACCG
CCTTCAGGCGTTCCTCGAACTCGCCGCGGAACTTGGCACCGCGATCAGCGCCCCCATGTCCAGGGCCAGCAGCAGCGCTTG
TCCTTGAGGCCGTCCGGCACTTCGCCGTTGATGATGACGCCCGCGATCAGCGCCCCCCATGTCCAGGGCCAGCAGCAGCGCGT
TTCGCCGATCAGCACCGGGTTGTTCTTGGTCCGCCGCTGCAGGACCTGGATGGTCCGGCGGATCTCGTCGTCGCGACCGA
TCACCGGGTCGAGCTTGCCTTCCTCGGCGCGCTTGGTCATGTCGACGGTGTACTTGTCCAGCGCCTTGCGCGACCCCTGCA
ACGTTCGGGTCGTTCACCGCTTCGCCGCCACCAGGATTGGCCACGGCATTCTCCAGCGCCTTGCGCGACACGCCCTGGCC
GAGCAGCAGCTTGCCGAGCCTGGTGTTCTCGTCCATCGCGGCCAACACCACCTCGCCGCACCCCCTTGC
TCTGCTGGGCCAGGCGGTCAGCCTGGTTGAGCAGGCGTGCGAGATCCTGGGACAGGTTCACGTCGCCGGTCGGCTCTGG
ATCTTCGGCAGCCGCTCGAGTTCTTTGTTGAGCACGCGCTGCCAAGACCGGCCAATACCAAGCCGACCTGCATCACCAGCGG
CTTGATCGAACCGCCTTGCTGCTCCAGCAGGGCGGAAAGCAGGTTCAACCGGCTCGATGGCCGATCGTCATCGCAACGG
CCAGGGACTGGGGCGTCGGAGAGCGCCAGTTGCAGCTTGCTGCTAAACGGTCATTCCTTCTTTTAT

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clpB protein SEQ ID NO: 279

MRIDRITSKLQLALSDAQSLAVGHDHPAIEPVHLLSALLEQQGGSIKPLLMQVGFDIAALRSGLNKELDALPKIQSPTGD VNLSQDLARLLNQADRLAQQKGDQFISSELVLLAAMDENTRLGKLLLGQGVSRKALENAVANLRGGEAVNDPNVEESRQA LDKYTVDMTKRAEEGKLDPVIGRDDEIRRTIQVLQRRTKNNPVLIGEPGVGKTAIVEGLAQRIINGEVPDGLKDKRLLAL DMGALIAGAKFRGEFEERLKAVLNELGKQEGRVILFIDELHTMVGAGKAEGAMDAGNMLKPALARGELHCVGATTLDEYR QYIEKDAALERRFQKVLVDEPSEEDTIAILRGLKERYEVHHGVSITDGAIIAAAKLSHRYITDRQLPDKAIDLIDEAASR IRMEIDSKPEELDRLDRRLIQLKIEREALKKEDDEATRKRLAKLEEDIVKLEREYADLEEIWKSEKAEVQGSAQIQQKIE QAKQEMEAARRKGDLESMARIQYQTIPDLERSLQMVDQHGKTENQLLRNKVTDEEIAEVVSKWTGIPVSKMLEGEREKLL RMEQELHRRVIGQDEAVVAVSNAVRRSRAGLADPNRPSGSFLFLGPTGVGKTELCKALAEFLFDTEEALVRIDMSEFMEK HSVARLIGAPPGYVGFEEGGYLTEAIRRKPYSVVLLDEVEKAHPDVFNILLQVLEDGRLTDSHGRTVDFRNTVVVMTSNL GSAQIQELAGDREAQRAAVMDAVNAHFRPEFINRIDEVVVFEPLAREQIAGIAEIQLGRLRKRLAERELSLELSQEALDK LIAVGFDPVYGARPLKRAIQRWIENPLAQLILAGKFAPGASISAKVEGDEIVFA.

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clpB DNA SEQ ID NO: 120

TACCTGACCGAGGCGATCCGCCGCAAGCCCTACTCGGTGGTGTGCTGCTGACGAGGTGGAGAAGGCCCATCCGGATGTATT
CAACATTCTCCTCCAGGTGCTCGAGGACGGACGCCTGACCGACACTCACGGCGTACGGTGGACTTCCGCAACACCGTGG
TGGTGATGACCTCCAACCTCGGTTCGGCGCAGATCCAGGAGCTGGCCGCAACGTGCCGCAGTGATG
GACGCGGTCAATGCGCACTTCCGTCCGGAATTCATCAACCGGATCGACGAAGTGGTGTTTCGAGCCGCTGGCTCGCGA
GCAGATCGCCGGCATCGCCGAGATCCAGCTCGGTCGCCAAGCGCCTGGCCGAGCTGAGCCTGGAACTGA
GCCAGGAGCCGCTGGACAAGCTGATTCCCGTCGGCTTCGACCCGGTCTATGGCGCACCCCGCTGAAGCGGCCATCCAG
CGCTGGATCGAGAACCCGCTGGCCAACTGATCCTGGCCGGCAAATTCGCGCCGGGTGCCAGTATCTCGGCGAAGGTGGA
AGGCGACGAGATCGTCTTCGCCTGA

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RS15

6,108 11,019 6,540 5,849 4,691 3,830 2,524 6,326 6,989 5,314 6,052 4,138 11,432 2,901 137 207 149 67 ខ 88 125 ads was interported and interp 0 56 53 57 6 60 56 outerimembrane andiperiplasm elt (cytoplasm) inner membrance outer membrane sand periplasing inner membrance outer membrane and periplasm cytoplasm cytoplasm cytoplasm cytoplasm spcU Putative transposase Hypothetical protein Putative transposase Hypothetical protein ExoU chaperone Acetyltransferase PA0981 / P. aeruginosa PAO1 PAO978741S SpcU / P. aeruginosa PA103 XF1753 / X. fastidiosa 9a5c PA0987 / P. aeruginosa PAO1 PP0651 / P. putida KT2440 Nolsigniticantsimilarity: 🛠 - 🖘 🧒 PA01 No significant similarity PA0979 / IS222 / P. aeruginosa 4E-62 (94) 4E-88 (85) 2E-75 (95) E-114 (99) 6E-50 (99) 3E-34 (49) AAN66276 AAG04370 AAG04368 AAC16024 AAF84562 PAN1938 PRSC2315 XCC3121, RSC2314 STY4665 PA1937,

RS11

RS09

RS07

RS05

RS03

RSO:

112/17

scytoplasm (8)

RS01

801

959

,280

pseudogene

57

ORF ID

Strand

Left end

Right end

ORI7 length

G+C content

Location prediction

Gene name

Gene function

Hypothetical protein

PA0977 / P. aeruginosa PAO1

Protein with the highest identity (Gene Name / Species Strain)

RNA-1/s/(PragnagnosalPAO)

E-value (%

GenBank

identity)

XénGWP, aegyginosa SG 17Meses

***(0.0 (04)) **

*AAG02084**

STN(4666)

XAC2196,

8E-37 (86)

AAG04366

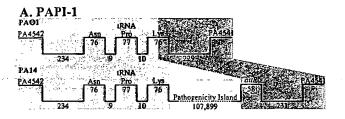
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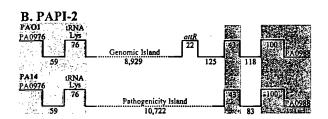
Proteins with lesser identity Cut off 30%

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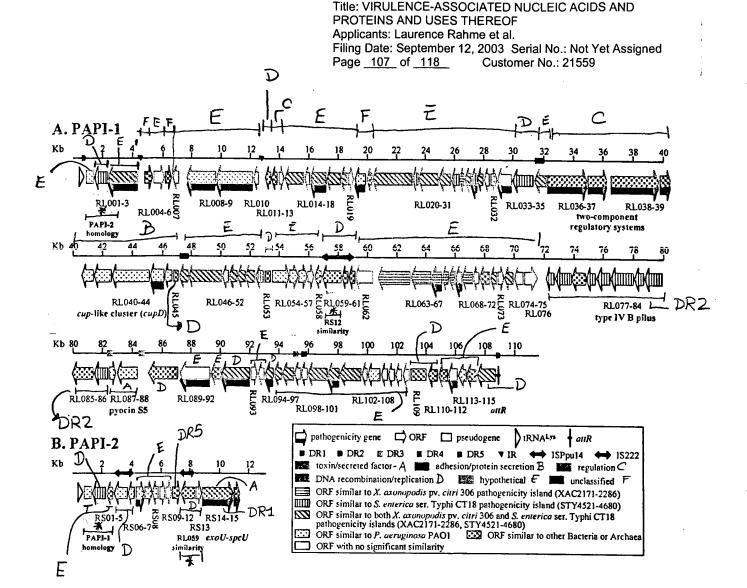
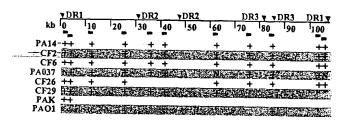


Figure 60

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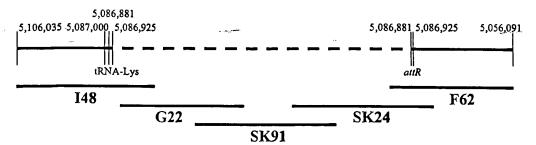
PROTEINS AND USES THEREOF Applicants: Laurence Rahme et al.

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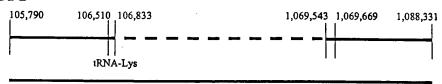
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### A. PAPI-1



#### B. PAPI-2



H44

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Strain	% Mouse	Growth in	Closest published homologue
name*	mortality [†]	Arabidopsis leaf [‡]	(organism / GenBank accession no.)
PA14	100	4.9 × 10 ⁶	
RL0038	41	$2.3\times10^5$	P. syringae pv. tomato DC3000 / AAO54371
RL008	38	$4.1\times10^6$	M. acetivorans C2A / AAM05538 and P. aeruginosa PAO1/ AAG05323
RL009	31	$1.3\times10^4$	P. aeruginosa PAO1 / AAG05327
RL016	100	$2.8\times10^4$	P. syringae pv. tomato DC3000 / AAO54383
RL020	50	$3.4\times10^5$	protein-disulfide isomerase, P. aeruginosa PAO1 / AAG04371
RL022	88	$3.3 \times 10^{6}$	P. syringae pv. tomato DC3000 / AAO54394
RL029	38	9.4 × 10 ⁴	P. aeruginosa C / AAN62148
RL033	25	4.9-x-10 ⁴	no significant similarity
RL036	44	$1.9\times10^5$	two-component sensor P. aeruginosa PA14 / AAM15532
RL037	43	$1.2\times10^5$	two-component regulator pvrR, P. aeruginosa PA14 AAM15533
RL038	31	$4.4\times10^4$	two-component sensor rcsC, S. typhimurium LT2 / AAL21172
RL039	31	$2.7\times10^5$	two-component regulator rcsB, E. coli O157:H7 EDL933 / AAG57352
RL043	75	$1.7\times10^6$	probable pili assembly chaperone cupA2, P. aeruginosa PAO1 / AAG05517
RL054	63	NT [¶]	P. aeruginosa PAO1 / AAG05610
RL062	78	NT [¶]	no significant similarity
RL065	63	$4.5\times10^5$	X. axonopodis pv. citri 306 / AAM37094
RL068	56	$2.6\times10^5$	no significant similarity
RL090	67	$2.7\times10^4$	no significant similarity
RL092	0	$1.3\times10^5$	topoisomerase I TopA, X. fastidiosa 9a5c (plasmid pXF51) / AAF85572
RL095	50	5.3x10 ⁵	single-stranded DNA binding protein Ssb, P. aeruginosa C / AAN62318
RL101	38	$1.8\times10^6$	Pseudomonas sp. B13 / CAD60668
RL112	38	$1.6\times10^4$	no significant similarity
RS06	100	1.8 × 10 ⁵	P. aeruginosa PAO1 / AAG04369

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	Positions	Length (bp)	Number of identical bp	Genes between the repeats
DRI	7444805 71087007108762	(63	==59 ===59	PAPHY(I088b)
DR2	31,587-32,248 47,100-47,761	662	654	two component regulatory systems and cup-like cluster (cupD)
-DR	8245774 <u>482</u> 4821 854296 <u>-854540</u>	248	2281	apyceineS5 and associated immunity protein.
DR4	95,301-95, <b>357</b> 95,358-95,414	57	50	none
DRS	1954767495/824 1957825495/881	in 58	-54	2000
IR	4,527-4,594 12,825-12,892		56	pathogenicity genes and Archaea homologous genes

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1S name	PAP	PI-1	PA	P1-2	Characteristics	of IS
	Position	Length (bp)	Position	Length (bp)	Original length (bp)	1S family
ISPpu14	56,778-59,119	2,341	7,034-7,999	966	2,383	1S66
IS222	-	-	2,980-4,201	1,222	1,232	IS3

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Function	Prototype name	Type IVB	Type IVA	Хер	Hxc	Hpl	Other homologues
		(PAPI-1 in PA14)	(PAO1)	(PAO1)	(PAO1)	(PAO1)	in PAO1 genome
ATPase :	pulE	RL082 (pilQ2)	pilB	xcpR	hxcRn	hplR	hvbA hx;A = v
		N NO AGREEM CON	pilit				
		A Section 1	pilUs 👫	. Piper			*****
Peptida <b>se</b>	pulO	RL079 (pilT2)?	pilD	pilD	pilD	pilD?	
Major pilin	or pulG:	RL080 (pilS2)1	pila	xcpT++	hxcT	hplT	
Minor pilin	pulH	RL077 (pilM2)	pilE	xcpU	hxcU	hplU	
	pulI	RL078 (pilV2)	fimU	xcpV	hxcV	hplV	
	pu <b>lJ</b>	RL083 (pilP2)	fimT	хсрW	hxcW	hplW	
	pulK	RL086 (pilL2)		хсрХ	hxcX	hplX	
Inner	puli	RL081 (pilR2)	pilG	хсрх	ixeS	liplS	xqM
membrane	PulC	RL084 (pilO2)		xcpP	hxcP		
protein !	PilL			etcpY.	lxcY		
	pul <b>M</b> i.			xcpZ-	hxcZ-		
Secretin	pulD	RL085 (pilN2)	pilQ	xcpQ	hxcQ		xqhA, xqhB, xqhC

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#### FIGURE 67

45

#### ORF 7 (SEQ ID NO: 280)

10

LEFGSATWTRTRDPMINSHLLYRLSYRGTSFFQPWTLPVLLDSRLRGAPFYGCARACOPSDPKSFSSFSTSDKTALPLHAAALSRLPDAHEKAPPKR
GFPCPPPKRSGEDDLVAFHLRRDTGTRREFAGODOLRQRVLDPALDGPLQRACAIDRVEADGNQLVQRLLAQFQAQLALQQATELDLGDAGDL
LASQRLEHHHFVDPVDEFRTEVRIDRVHHCGTLRLAVAGQLLDLRRTEVGGHHHHGVAEVHRTPVTVGQASVLEHLEENVEYIRMGLLHLVQQHHRV
GLAADRLGQVAAFLEADVARRRADQAGHRVFLHELGHIYPHQRLLGIEEELGQRLAQLGLAHPGRAEEEERAARPVRIGEAGARTAHGVGHGDYRLV
LADHSPMQLLLHAQQLLALALEHLRHRDTGPLGNHFGDFLVGHLVAQQLVLGLAVLVDHLQAAFQVRDGLVLDARHALEVALAPRRLHLLLGLLDLL
LDLRRALHLGLLGLPDLLEVGVFALELDDILLQLGQALPGGFVVFLLQRLALDLQLDQATVETIQFLRLGVDLHADAAGGLVDQVDGLVRQLPIGDV
AVRQLGRGDDRAVGDAHPVVHFIAFLEATEDGDGVFLARFVHQHLLEAALQRGILLDVLAILVEGSSTDAVQLAARQSRLEHVAGVHGTFRLAGADH
GVQFVDEQDDPAFLLAQFVEDRLQAFLELAAELGTGDQRPHVQGQQALVLEAVRHFAVDDALGQALDDGGLADAGFADQHRVVLGPPLQDLDGPADL
VVATDHRVELAFLGALGHVDGVLVQRLARLLDVRVVHRFAATQVCHGILQRLARHALAEQQLAEPGVLVHRGQQYQLAGGDELVALLLGQAVSLVQQA
CEILGQVHVAGRALDLRQRVEFFVEAAAQGGDIEADLHQQGLDRTALLLEQGGKQVHRLDGRMVMANGQGLGVGERQLQLAGQTVYSHGSSFLL

15 ORF7 (SEQ ID NO: 281) AACCCTGGACGCTTCCGGTGTTGCTGGATTCGCGTCTCAGAGGCGCGCCCATTTTACGGATGCGCGCGGGCATGTCAACCCTCTGATCCAAAAAGTTT TTCTTCTTTTTCCACGACGACAAAACGGCCCTTCCACTGCATGCGGCAGCGCTCTCGCGCCTACCGGACGCCCATGAAAAAGCCCCGCCGAAGCGG GGCTTTCCCTGTCCGCCCCGAAGAGGTCAGGCGAAGACGATCTCGTCGCCTTCCACCTTCGCCGAGATACTGGCACCCGGCGCGAATTTGCCGGCC 20 AGGATCAGTTGCGCCAGCGGGTTCTCGATCCAGCGCTGGATGGCCCGCTTCAGCGGGCGTGCGCCATAGACCGGGTCGAAGCCGACGGCAATCAGCT TGTCCAGCGCCTCCTGGCTCAGTTCCAGGCTCAGCTCGCGCCAGGCGCTTGCGCAGGCGAGCCGAGCTGGATCTCGGCGATGCCGGCGATCTC  ${\tt TGCGCCTCGCGGTCGCCGGCCAGCTCCTGGATCTGCGCCGAACCGAGGTTGGAGGTCATCACCACCGCGTGTTGCGGAAGTCCACCGTACGCCCGT}$ GACTGTCGGTCAGGCGTCCGTCCTCGAGCACCTGGAGGAGAATGTTGAATACATCCGGATGGGCCTTCTCCACCTCGTCCAGCAGCACCACCGAGTA 25 GGGCTTGCGGCGGATCGCCTCGGTCAGGTAGCCGCCTTCCTCGAAGCCGACGTAGCCCGGAGGCGCCGCCGATCAGGCGGGCCACCGAGTGTTTCTCC ATGAACTCGGACATATCTATCCGCACCAGCGCCTCCTCGGTATCGAAGAGGGAACTCGGCCAGCGCCTTGCACAACTCGGTCTTGCCCACCCCGGTCG  $\tt CTGGCCGATCACTCGCCGATGCAGCTCCTGCTCCATGCGCAGCAGCTTCTCGCGCTCGCCCTCGAGCATCTTCGACACCGGGATACCGGTCCACTTGCTCGACTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCGACACCGGGATACCGGTCCACTTGCTCACTTGCTCACTTCGACACCGGGATACCGGTCCACTTGCTCACTTGCTCACTTCGACACCGGGATACCGGTCCACTTGCTCACTTGCTCACTTCGACACCGGGATACCGGTCCACTTGCTCACTTGCTCACTTGCTCACTTCGACACCGGGATACCGGTCCACTTGCTCACTTGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCAC$  ${\tt GAAACCACTTCGGCGATTTCCTCGTCGGTCACCTTGTTGCGCAGCAACTGGTTCTCGGTCTTGCCGTGCTGGTCGACCATCTGCAGGCTGCGTTCCA}$ 30 GGTCCGGGATGGTCTGGTACTGGATGCGCGCCATGCTCTCGAGGTCGCCCTTGCGCGCCGCCCCCCATCTCCTGCTTGGCCTGCTCGATCTTCTG AGCTTGGCCAGGCGCTTCCTGGTGGCTTCGTCGTCTTCTTCAGCGCCTCGCGCTCGATCTTCAGCTGGATCAGGCGACGGTCGAGACGATCCA GTTCCTCCGGCTTGGAGTCGATCTCCATGCGGATGCGGCTGGCGGCCTCGTCGATCAGGTCGATGGCCTTGTCCGGCAGTTGCCGATCGGTGATGTA 35 ATGGTGTCTTCCTCGCTCGGTTCGTCCACCACCACCTTCTGGAAGCGGCGCTCCAGCGCGCATCCTTCTCGATGTACTGGCGATACTCGTCGAGGG TAGTAGCACCGACGCAGTGCAGCTCGCCGCCGCCCCAGAGCCCGCTTGAGCATGTTGCCGGCGTCCATGGCACCTTCCGCCTTGCCGGCGCCCGACCAT 40 GTCGTCGCGACCGATCACCGGGTCGAGCTTGCCTTCCTCGGCGCGCTTGGTCATGTCGACGGTGTACTTGTCCAGCGCCTGGCGCGACTCCTCGACG TGCGAGATCCTGGGACAGGTTCACGTCGCCGGTCGGGCTCTGGATCTTCGGCAGCGCGTCGAGTTCTTTGTTGAGGCCGCTGCGCAGGGCGGCGATA TCGAAGCCGACCTGCATCAGCAGGGGCTTGATCGAACCGCCTTGCTCGTGCTCGAGCAGGGCGGAAAGCAGGTGCACCGGCTCGATGGCCGGATGGTCAT

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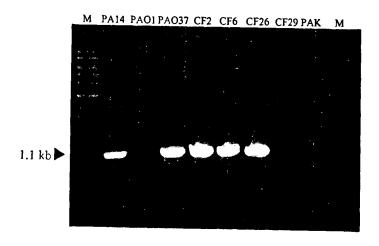
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#### FIGURE 68 (SEQ ID NO: 121)

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#### FIGURE 70A

CLUSTAL W (1.82) multiple sequence alignment

	•
CF2 (SEQ ID NO: 122)	GATGAAGG-ACCCGAGCGGAACATCCATCTCAC 32
PAO37 (SEO ID NO: 123)	
	GATGAAGG-ACCCGAGCGGAACATCCATCTCAC 32
CF6 (SEQ ID NO: 124)	GATGAAGGCACCCGAGCGGAACATCCACCTCAC 33
PA14 (SEQ ID NO: 125)	TTTCCGGCACACCCTGGCCACCGACTTGATGAAGGCACCCGAGCGGAACATTCACCTCAC 60
CF26 (SEQ ID NO: 126)	GATGAAGG-ACCCGAGCGGAACATCCACCTCAC 32
	******* ******** ** ****
CDC.	0110magamagamagamagamagamagamagamagamagamag
CF2	GAAGTGCCTGCTCAACCACTCGAATATCCAGACCACCATGAGCTACATCGAGGCCGACTA 92
PAO37	GAAGTGCCTGCTCAACCACTCGAATATCCAGACCACCATGAGCTACATCGAGGCCGACTA 92
CF6	GAAGTGCCTGCTCAACCACTCGAATATCCAGACCACCATGAGCTACATCGAGGCCGACTA 93
PA14	GAAGTGCCTGCTCAACCACTCGAATATCCAGACCACGATGAGCTACATCGAGGCCGACTA 120
CF26	GAAGTGCCTGCTCAACCACTCGAATATCCAGACCACGATGAGCTACATCGAGGCCGACTA 92
	******************
CTO.	00.00.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
CF2	CGACCACATGCGTGCCGTGCTGCATGCCAGAAGCCTGGCCCAAGGAGCGCTGGAGAACGT 152
PAO37	CGACCACATGCGTGCCGTGCTGCATGCCAGAAGCCTGGCCCCAAGGAGCGCTGGAGAACGT 152
CF6	CGACCACATGCGTGCCGCGCATGCCAGAAGCCTGGCCCAAGGAGCGCTGGAGAACGT 153
PA14	CGATCACATGCGTGCCGTGCTGCATGCTAGAAGCCTGGCCCAAGGCGCGCTGGAGAATGT 180
CF26	CGATCACATGCGTGCCGTGCTGCATGCTAGAAGCCTGGCCCAAGGCGCGCTGGAGAATGT 152
	*** ******************************
CES	CACCAACCTCCATTACACCCCCTTCCCCCCAACCCCAAACCCCAAACCCAAAACCCAAAACCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAA
CF2	CAGGAAGGTGGATTACAGCGGCTCCCCGCAAGCCTCTGCCAAACCGAAGCCATGCGGGCA 212
PAO37	CAGGAAGGTGGATTACAGCGGCTCCCCGCAAGCCTCTGCCAAACCGAAGCCATGCGGGCA 212
CF6	CAGGAAGGTGGATTACAGCGGCTCCCCGCAGGCCTCTGCCAAACCGAAGCCATGCGGGCA 213
PA14	CAGGAAGGTGGATTACAGCGGCTCCCCGCAAGCCTCTGCCAAACCGAAGCCATGCGGGCA 240
CF26	CAGGAAGGTGGATTACAGCGGCTCCCCGCAAGCCTCTGCCAAACCGAAACCATGCGGGCA 212
	***************************
CF2	ACCTCTCGCTCGAATGGGTGAAGTACCGCCGCCGGAGGCCAGGACAGAACCTGCAGAACC 272
PAO37	
	ACCTCTCGCTCGAATGGGTGAAGTACCGCCGCGGAGGCCAGGACAGAACCTGCAGAACC 272
CF6	ACCTCTCGCTCGAATGGGTGAAGTACCGCCGCCGGAGGCCAGGACAGAACCTGCAGAACC 273
PA14	ACCTCTCGCTCGAGTGAGTGAAGCGCCGCCACCGGAGGCCAGGACAGAGCCTGCAGAACC 300
CF26	ACCTCTCGCTCGAGTGAGTGAAGCGCCGCCACCGGAAGCCAGGACAGAGCCTGCAGAACC 272
	******** ** ***** ** ***** ***** ******
CF2	AAGGGAGCACATACCAGGGACAGGCATTCAGGGAGGTCCAACCGTGCGGGAAGAAGC 329
PAO37	AAGGGAGCACATACCAGGGACAGGCATTCAGGGAGGTCCAACCGTGCGGGAAGAAGC 329
CF6	AAGGGAGCACACACGGGACAGGCATTCAGGGAGGTCCAACCGTGCGGGAAGAAGC 330
PA14	
	AAGGGAGCACACGCCAGGGACAGGCATTCAGGGAGGTCCAACCGCGTGGGAAGCAGATGC 360
CF26	AAGGGAGCACACCAGGGACAGGCATTCAGGGAGGTCCAACCGAGTGGGAAGCAGAAGC 332
	***************************************
CF2	GCTACCACAGCCACCTGACACCTTCGACCAAAGCGTGCTGTTCACTCTGATGGCTCAACA 389
PAO37	GCTACCACAGCCACCTGACACCTTCGACCAAAGCGTGCTGTTCACTCTGATGGCTCAACA 389
CF6	GCTACCACAGCCACCTGACACCTTCGATCAAAGCGTGCTGTTCACTCTGATGGCTCAACA 390
PA14	GCTACCACAGCCACCTGACACCTTCGAACCAAGCGTGCTGTTCACTCTGATGGCTCAAAA 420
CF26	GCTACCACAGCCACCTGACACCTTCGAGCAAAGCGTGCTGTTCACTCTGATGGCTCAAAA 420
	**************************************
CF2	CTTATCGAACCGTGCCGCCTCGGCATCCGCGGCTCCCGCTGCAACAAGCGGATCTGGTGG 449
PAO37	CTTATCGAACCGTGCCGCCTCGGCATCCGCGGCTCCCGCTGCAACAAGCGGATCTGGTGG 449
CF6	CTTATCGAACCGTGCCGCCTCGGCATCCGCAGCTCCCGCTGCAACAAGCGGATCTGGTGG 450
PA14	CTTATCGAACCGTGCCGCCTCGGCATCCGCGGCTCCCGCTGCAACAAGCGGATCAGGCGG 480
CF26	CTTATCGAACCGTGCCGCCACGACATCTGCGGCTCCCGCCGCAACCAGCGGATCTTGTAG 452
• •	**************** ** *** ** ***** **** ****
CF2	ATGGGGATCTACTGCCCGAAGCAGTCTCGCCTAGCGATACCGATACTGAAGGGCCGGCTA 509
PAO37	ATGGGGATCTACTGCCCGAAGCAGTCTCGCCTAGCGATACCGATACTGAAGGGCCGGCTA 509
CF6	ATGGGGATCTACCGCCCGAAGCAGTCTCGCCTAGCGATACCGGTACTGAAGGGCCGGCTA 510
PA14	ATGGGGATCTGCCGCCCGAAGCAATCTCGCCTAGCGATACCGGTACTGA-GGGCCGGCTA 539
CF26	ATGGGGATCTGCCGCCCGAAGCAGCCTCGCCTAGCGATACCGGTACTGAGGGGCCCGGCTA 512
	******** * ********* ******* ***** *****

Title: VIRULENCE-ASSOCIATED NUCLEIC ACIDS AND PROTEINS AND USES THEREOF

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FIGURE 70B	,
CF2	CCGGACGAAAGGTAGCCGCGCCTCCCAGCAGTTCGCTAGGCCTGTAAGAAAAATCTGGAA 569
PAO37	CCGGACGAAAGGTAGCCGCCCCCCAGCAGTTCGCTAGGCCTGTAAGAAAAATCTGGAA 569
CF6	CCGGACGAAAGGTAGCCGCGCCTCCCAGCAGTTCGCTAGGCCTGTAGGAAAAATCTGGAA 570
PA14	CCGGACGAAAGGTAGCCGTGCCTTCCAGCAGATCGTTAGGCCTGTAGGAAAAATCTGGAA 599
CF26	CCAGACGAAAGGTAGCCGCGCCTCCCAGCAGATCGCTGGGCCTGTAGGAAAAATCTGGAA 572
	** ********* *** *** **** *** ** * * ****
CF2	TTACCGAGAGCGCCTGGATTCCAGCGCCGGCATGCTGGCAGAGCCC-CGCAGTTTCACGG 628
PAO37	TTACCGAGAGCGCCTGGATTCCAGCGCCGGCATGCTGGCAGAGCCC-CGCAGTTTCACGG 628
CF6	TTACCGAGAGCGCCTGGATTCCAGCGCCGGCATGCTGGCAGGGCCC-CGCAATTTCAAGG 629
PA14	TTACCGAGAGCGCCTGGATTCCAGCGCCGGCATGCTGGCAGAGCCAGCGCAATTTCAAGG 659
CF26	TTACCGAGAGCGCCTGGATTCCAGCGCCGGCATGCTGGCAGAGCCC-CGCAATTTCACGG 631
	***************
CF2	CCAAAACCGCAGTACCCTCTGTAATCGCTGATTACGTCGGGGGGCGCATTGCTACGCCTGC 688
PAO37	CCAAAACCGCAGTACCCTCTGTAATCGCTGATTACGTCGGGGGGCGCATTGCTACGCCTGC 688
CF6	C-GAAACCGCAGTACCCTCTGTAATCGCTGATTACGTCGAGGGCACATTGCTACGCCTGC 688
PA14	CCAATACCACAGTACCCTCTGTAATCGCTGATTACGTCGGGGGGGCGCATTGCTACGCCTGC 719
CF26	C-AAAACCGCAGTACCCTCTGTAATCGCTGATTACGTCGGGGGGCACATTGCTACGCCTGC 690
	* * *** ****************** **** ****
CF2	AGAA-TGGTTTCAGGGCCTTANAAACAGAAAAGCCCACCTTAAATAGGCGGGCTATT-CC 746
PAO37	AGAAATGGTTTCAGGGCCTTAGAAACAGAAAAGCCCACCTAAATAGGCGGGCTATT-CC 747
CF6	AGAA-TGGTTTCAGAGCCT-GAAAACAGAAAAGNCCACC-TAAATAGGCGGGCTATTTCC 745
PA14	AGAA-TGGTTTCAGGGCCTTAGAAACAGAAAAGCCCACC-TAGAAAGGCGGGCTATT-CC 776
CF26	AGAA-TGGTTTCAGAGCCTTANAAACAGAAAAGCCCACC-TAGATAGGCGGGCTATT-CC 747
•	**** ****** **** **** ***** **** ** * *
	•
CF2	ATATT-GACATCACG-TCAATGCGGGCCTAATGTTCGGCCCAGACGGCTGCTGG 798
PAO37	ATATT-GACATCACG-TCAATGCGGGCCTAATGTTCGGCCCANACGGCTGCTGG 799
CF6	ATATTTGACATCCCG-TCAATGCGGGGCCCTAATGGTTCGGGCCCANACGGCTTGCTTGG 804
PA14	ATATT-GACATCACG-TCAATGCGGGCCTAATGTTCGGCCCAGACGGCTGCTAG 828
CF26	ATATT-GACATCACGGTCAATGCGGGGCTAATGTTC-GGGCCCANACGGNTGCAA 800
	**** ***** ** ** ** **** * * * * * * * *